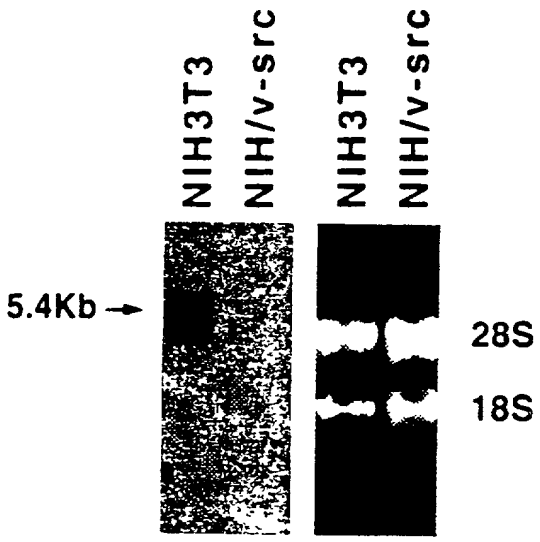


FIG.1

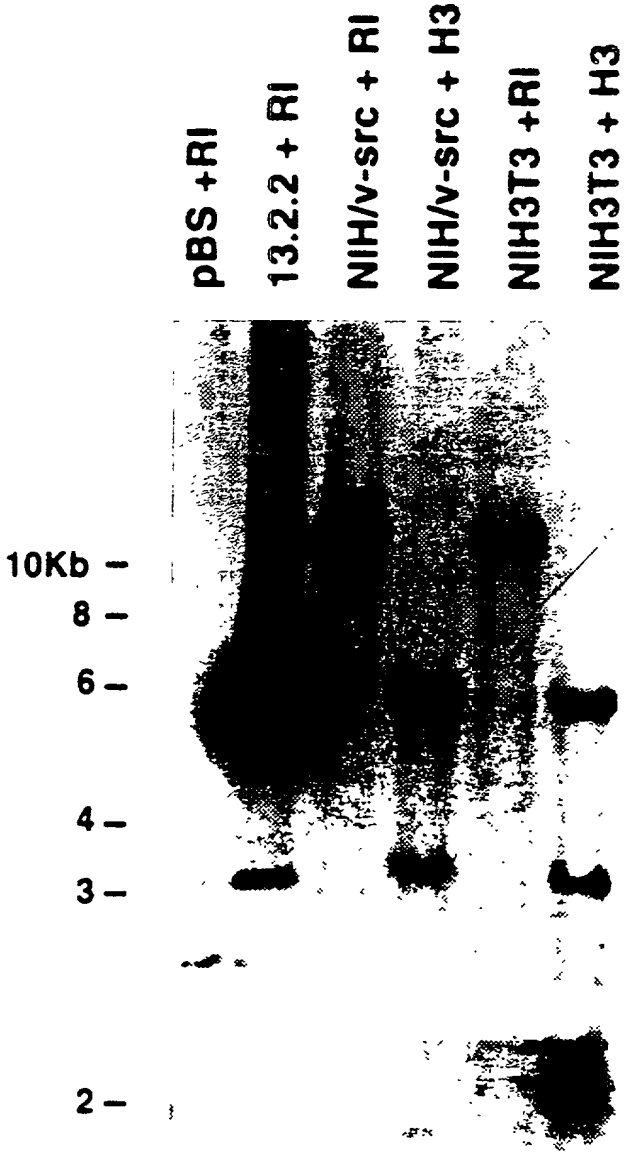

pBS +RI
13.2.2 + RI
NIH/v-src + RI
NIH/v-src + H3
NIH3T3 +RI
NIH3T3 + H3
10Kb
8
6
4
3
2

FIG.2A

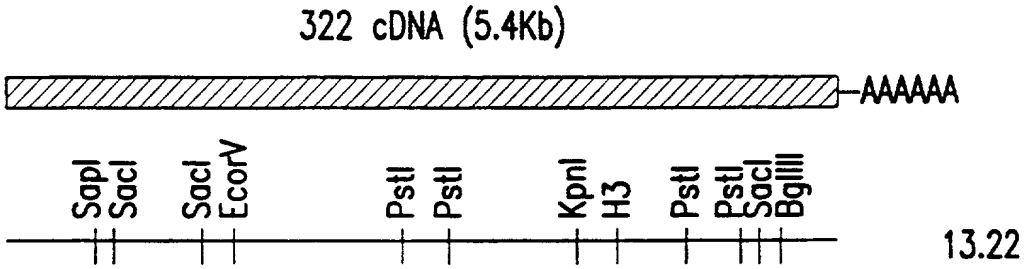

322 cDNA (5.4Kb)
AAAAAA
SapI
SacI
SacI
EcorV
PstI
PstI
KpnI
H3
PstI
PstI
SacI
BglII
13.22

FIG.2B

```
       ggaaaagacagagccagcctcggaggagcaggagccggcagaagacacagaccaggccag    60
       gttgtcagcagactacgagaaggtggagctgcctttggaagaccaggttggtgacctgga   120
       ggcatcgtcagaggagaagtgtgctcctttggcaacggaagtgtttgatgagaagatgga   180
                                                                 M  E     2

181    agcccaccaagaagttgttgcagaggtccacgtgagcaccgtggagaagacagaggagga   240
3       A  H  Q  E  V  V  A  E  V  E  V  S  T  V  E  K  T  E  E  E    22

241    gcagggaggaggaggagaggctgaaggggcgtggtggtagaaggaacaggagaatcctt   300
23      Q  G  G  G  G  E  A  E  G  G  V  V  V  E  G  I  G  E  S  L    42

301    gccccctgagaaactggctgagccccaggaggtcccccaggaagctgagcctgctgagga   360
43      P  P  E  K  I  A  E  P  Q  E  V  P  Q  E  A  E  P  A  E  E    62

361    gctgatgaagagcagagagatgtgtgtctctggaggagaccacactcaactgacagacct   420
63      I  M  K  S  R  E  M  C  V  E  G  G  D  H  T  Q  L  T  D  L    82

421    aagtcctgaagagaagacgctgcccaaacacccagaaggcattgtcagtgaggtggagat   480
83      S  P  E  E  K  T  L  P  K  H  P  E  G  I  V  S  E  V  E  M   102

481    gctgtcctctcaggaaagaatcaaggtacagggaagtcccttgaagaaactcttcagtag   540
103     L  S  S  Q  E  R  I  K  V  Q  G  S  P  L  K  K  L  F  S  S   122

541    ctcaggcttaaagaagctgtctgggaagaagcagaaggggaaacgaggaggtgggggaga   600
123     S  G  L  K  K  L  S  G [K  K  Q  K] G  K  R  G  G  G  G  D   142

601    cgaagagcctggagaataccaacacattcacaccgaatccccagagagtgctgatgagca   660
143     E  E  P  G  E  Y  Q  H  I  H  T  E  S  P  E  S  A  D  E  Q   162
```

FIG.3A

```
661  gaagggagagagctctgcgtcgtcccccgaggagcctgaggagaccacgtgtctggagaa  720
163   K  G  E  S  S  A  S  S  P  E  E  P  E  E  I  I  C  L  E  K   182

721  agggccgctggaagcacccaggatggggaagctgaggaaggaactacttcgtggagagaa  780
183   G  P  L  E  A  P  R  M  G  K  L  R  K  E  L  L  R  G  E  K   202

781  gaagaggaaggatcactccctgggcatccttcaaaaagatggtgacacccaagaaacggt  840
203   K  R  K  D  H  S  L  G  I  L  Q  K  D  G  D  I  Q  E  T  V   222

841  ccgaagaccttctgagagtgacaaggaggaagagctggagaaggtcaagagcgccacctt  900
223   R  R  P  S  F  S  D  K  F  E  E  L  F  K  V  K  S  A  I  L   242

901  gtcctccactgatagcacagtgtcagaaatgcaagatgaagtcaaaactgttggtgagga  960
243   S  S  T  D  S  T  V  S  E  M  Q  D  E  V  K  I  V  G  E  E   262

961  acaaaagccagaggaaccaaagcgtagggtggatacttcagtgtcttgggaagcactgat  1020
263   Q  K  P  E  E  P  K  R  R  V  D  T  S  V  S  W  E  A  L  I   282

1021 ttgtgtcggatcatccaagaagagagcaaggaaggcatcctcttcagatataagagggcc  1080
283   C  V  G  S  S  K  K  R  A  R  K  A  S  S  S  D  I  R  G  P   302

1081 aaggacactgggaggggacagtcacagagcagaggaggccagcaaagacaaagaagccg  1140
303   R  T  L  G  G  G  Q  S  Q  S  R  G  G  Q  Q  R  Q  R  S  R   322

1141 aacagacgctgttcctgccagcacccaggagcaggaccaagcgcaaggaagttcctcacc  1200
323   T  D  A  V  P  A  S  T  Q  E  Q  D  Q  A  Q  G  S  S  S  P   342

1201 cgagccagcgggaagcccttccgaaggggaaggtgtctccacttgggagtcatttaaaag  1260
343   E  P  A  G  S  P  S  E  G  E  G  V  S  T  W  E  S  F  K  R   362
```

FIG.3B

(15 of 90)

```
1261  attagtcactccaagaaaaaaatccaagtcaaaactggaagagaaagaagccggaaggac  1320
363   L  V  T  P  R  K  K  S  K  S  K  L  E  E  K  E  A  G  R  T   382

1321  tctagttgtaggagcaggttgtccactgagatcgaaccgtgtagagaagaatcttgggtt  1380
383   L  V  V  G  A  G  C  P  L  R  S  N  R  V  E  K  N  I  G  F   402

1381  tccattaagaaattcatccccggacggcggaagaaaagggcagatgggaaggcaagaaca  1440
403   P  I  R  N  S  S  P  D  G  G  R  K  G  Q  M  G  R  Q  E  Q   422

1441  agccactgtggaagactcagggccagtggagataaatgaggacgagcctgatgtcccagc  1500
423   A  T  V  E  D  S  G  P  V  E  I  N  E  D  E  P  D  V  P  A   442

1501  agtcgtgcctctgtctgagtatgatgcagtggagagggagaagatggaagcccaggggaa  1560
443   V  V  P  L  S  E  Y  D  A  V  E  R  F  K  M  E  A  Q  G  N   462

1561  tgcggagctgcccagctgctggggctgtgtagtgtccgaggagctcagtaagactctggt  1620
463   A  E  L  P  S  C  W  G  C  V  V  S  E  E  L  S  K  T  L  V   482

1621  ccacactgtgagtgtcgcagtcattgatgggaccagggcagtcaccagtgtcgaagagcg  1680
483   H  T  V  S  V  A  V  I  D  G  T  R  A  K  T  S  K  E  E  R   502

1681  gtctccttcgtggatatccgcttccgtaacagaacctcttgaacacacagcgggagaagc  1740
503   S  P  S  W  I  S  A  S  V  T  E  P  L  E  H  T  A  G  E  A   522

1741  catgccacctgttgaagaggtcactgaaaaagacatcattgcagaagaaactcctgtgct  1800
523   M  P  P  V  E  E  V  T  E  K  D  I  I  A  E  E  T  P  V  L   542

1801  cacccagacgttaccagagggtaaagatgcccatgacgacatggtcaccagtgaagtgga  1860
543   T  Q  T  L  P  E  G  K  D  A  H  D  D  M  V  T  S  E  V  D   562
```

FIG.3C

1861	tttcacctcagaagctgtgacagccacagagacctcagaggctctccgtactgaagaagt	1920
563	F T S E A V T A T F T S E A L R T E E V	582
1921	taccgaagcatcgggggccgaagagaccacagacatggtgtccgcagtttcccagctgac	1980
583	T E A S G A E E T T D M V S A V S Q L T	602
1981	tgactccccagacaccacagaggaagccaccccagttcaggaggtagagggtggtgtgct	2040
603	D S P D T T E E A T P V Q E V E G G V L	622
2041	agatacagaagaagaggagcgccagacgcaggccatcctccaagccgttgcagacaaggt	2100
623	D I E E F F R Q T Q A I I Q A V A D K V	642
2101	gaaagaggagtcccaggtgcctgcaacccagactgtgcagagaacggggtcaaaagcact	2160
643	K E E S Q V P A T Q T V Q R T G S K A L	662
2161	ggagaaggttgaggaggtagaggaggactccgaagtgctggcttcggagaaagagaagga	2220
663	E K V F F V F E D S E V L A S E K E K D	682
2221	cgttatgccgaaaggacccgtgcaggaagctggagctgagcatcttgcacagggctctga	2280
683	V M P K G P V Q E A G A E H L A Q G S F	702
2281	gactggacaggctactccagagagccttgaagttcctgaagtcacagcagatgtagacca	2340
703	T G Q A T P E S L E V P E V T A D V D H	722
2341	tgtcgccacgtgccaggttatcaagctccagcagctgatggaacaggccgtggcccctga	2400
723	V A T C Q V I K L Q Q L M E Q A V A P E	742
2401	gtcatccgaaaccttgacagacagtgagacaaatggaagcactcccttagcagattcaga	2460
743	S S E T L T D S E T N G S T R L A D S D	762

FIG.3D

(74 of 90)

```
2461  cactgcagatgggacacagcaagatgaaaccattgacagccaggacagtaaagccactgc  2520
763    T  A  D  G  T  Q  Q  D  E  T  I  D  S  Q  D  S  K  A  T  A   782

2521  agctgtcaggcagtcacaggtcacagaagaagaggcggctactgctcagaaagaggagcc  2580
783    A  V  E  Q  S  Q  V  I  E  E  E  A  A  I  A  Q  K  E  E  P   802

2581  ttcgacactacctaataatgttccagcccaggaagaacatggggaagaaccaggaagaga  2640
803    S  T  L  P  N  N  V  P  A  Q  E  E  H  G  E  E  P  G  R  D   822

2641  tgttcttgaacctacacagcaagagcttgctgctgcagccgtgcccgtctggcaaaagac  2700
823    V  L  E  P  T  Q  Q  E  L  A  A  A  A  V  P  V  W  Q  K  T   842

2701  tgaggtgggtcaagagggtgaggttgactggttggatggagaaaaagtcaaagaagaaca  2760
843    E  V  G  Q  F  G  E  V  D  W  I  D  G  E  K  V  K  E  E  Q   862

2761  ggaggtgtttgtacactctggacccaacagtcaaaaggctgctgatgtgacatatgacag  2820
863    E  V  F  V  H  S  G  P  N  S  Q  K  A  A  D  V  T  Y  D  S   882

2821  tgaagtgatgggagtggccgggtgtcaggaaaaggagagtactgaagtgcagagtcttag  2880
883    E  V  M  G  V  A  G  C  Q  E  K  E  S  T  E  V  Q  S  L  S   902

2882  cctggaggagggagagatggaaactgacgttgaaaaggagaaaagggagacaaagccaga  2940
903    L  E  E  G  E  M  E  T  D  V  E  K  E  K  R  E  T  K  P  E   922

2941  gcaagtgagtgaagaaggtgagcaggaaacagccgctcctgagcatgaaaggaactacgg  3000
923    Q  V  S  E  E  G  E  Q  E  T  A  A  P  E  H  E  R  N  Y  G   942

3001  gaagccagtcctgacacttgacatgcccagctcagagaggggggaaggcactgggaagcct  3060
943    K  P  V  L  T  L  D  M  P  S  S  E  R  G  K  A  L  G  S  L   962
```

FIG.3E

```
3061  tggaggaagccctlctctcccagaccaagacaaagcaggttgcatagaggttcaagttca  3120
 963   G  G  S  P  S  I  P  D  Q  D  K  A  G  C  I  E  V  Q  V  Q    982

3121  aagcctggacacaacagtcactcaaacagcagaagctgtggaaaaggtcatagaaacggt  3180
 983   S  I  D  I  T  V  T  Q  T  A  E  A  V  F  K  V  I  E  T  V   1002

3181  tgtgatttcagagacaggtgaaagtccagagtgtgtaggtgcacacttattaccagctga  3240
1003   V  I  S  E  T  G  E  S  P  E  C  V  G  A  H  L  I  P  A  E   1002
                              →Zn-finger←
3241  gaagtcctctgcaacgggtggccactggactcttcagcatgcagaggacacggtacccct  3300
1023   K  S  S  A  T  G  G  H  W  T  L  Q  H  A  F  D  T  V  P  L   1042

3301  ggggcctgagtctcaggcagaatccatcccaatcatagtaactcctgctcctgaaagcac  3360
1043   G  P  F  S  Q  A  I  S  I  P  I  I  V  T  P  A  P  E  S  T   1062

3361  cctacatcctgacctacaaggagaaataagcgcatcccagagagagcgatcagaggaaga  3420
1063   L  H  P  D  L  Q  G  E  I  S  A  S  Q  R  E  R  S  E  E  E   1082

3421  ggacaagccagatgctggtcctgatgctgacggcaaggagagtacagcaatcgacaaagt  3480
1083   D  K  P  D  A  G  P  D  A  D  G  K  E  S  T  A  I  D  K  V   1102

3481  cctcaaggctgaacctgagatcctggaacttgagagtaagagcaacaagattgtgctgaa  3540
1103   L  K  A  E  P  E  I  L  E  L  E  S  K  S  N  K  I  V  L  N   1122

3541  cgtcattcagacagccgttgaccagttcgcacgtacagaaacagcccccgaaactcatgc  3600
1123   V  I  Q  T  A  V  D  Q  F  A  R  T  E  I  A  P  E  T  H  A   1142

3601  ttatgattcacagacccaggttcctgcaatgcgcttggacagcagggagcccaacagatg  3660
1143   Y  D  S  Q  T  Q  V  P  A  M  R  L  D  S  R  E  P  N  R  C   1162
```

FIG.3F

```
3661  ctggacaaaaatgaaagttgccaagatgaaacacccagtgccgcagcccagagaggactt  3720
1163   W  I  K  M  K  V  A  K  M  K  H  P  V  P  Q  P  R  E  D  L   1182

3721  gcaagtcctgaccgttctggaggcatggctcagctcggaaatgcttgccgcgcttgcagt  3780
1183   Q  V  L  T  V  L  E  A  W  L  S  S  E  M  L  A  A  L  A  V   1202

3781  tgaaagcgccggtgtcaaagtaagcattgagaagctgcctcctcaacccaaagatcaaaa  3840
1203   E  S  A  G  V  K  V  S  I  E  K  L  P  P  Q  P  K  D  Q  K   1222

3841  ggagcatgctgctgatggccctcagctccaaagcttagcccaggcagaggcagtgtctgg  3900
1223   E  H  A  A  D  G  P  Q  L  Q  S  I  A  Q  A  E  A  V  S  G   1242

3901  aaacctaaccaaagaatccccagacaccaacggaccaaagctaaccgaggagcgatgccc  3960
1243   N  I  I  K  F  S  P  D  I  N  G  P  K  L  I  F  E  R  C  P   1262

3961  ccaaaagttgaggtccaggaagaagaaatgtctaccaagtcagtcaaagagaacaaggcc  4020
1263   Q  K  I  R  S  R  K  K  K  C  L  P  S  Q  S  K  R  T  R  P   1282

4021  caggcagaagaggacctgcaggagccaaagggagacctggcagaatcctaagatgttagt  4080
1283   R  Q  K  R  T  C  R  S  Q  R  E  T  W  Q  N  P  K  M  L  V   1302

4081  tgctcattgtacatctgtaagaccagaatgtgaaaacaagtcacagaacaagatgctgct  4140
1303   A  H  C  T  S  V  R  P  E  C  E  N  K  S  Q  N  K  M  L  L   1322

4141  gttgggaccttggaccaagatttcagagcccatgagatccagagagcagggccgtccaat  4200
1323   L  G  P  W  T  K  I  S  E  P  M  R  S  R  E  Q  G  R  P  M   1342

4201  gatttccacccagtagagcaccccgacaattctgaggcttcatcgggagctagagccagc  4260
1343   I  S  T  Q  *                                               1346
```

FIG.3G

(10 of 90)

```
4261  taacatttcctcgtttcaagactgcctttgatttgccccttgatgccgtccgtgtatttc  4320
4321  ggatttaaggtcctgcgttctcaacctggaaccaattctgccatacctagttccacttct  4380
4381  caaactggagcatcctcctttatgtatttatatgtatgttttatgtagtcctcctcctgt  4440
4441  acctattgtatatttttttctaacgtttaagcacatgcttttgtattatgcaatatata  4500
4501  acgggtgtgcagccatagcgacgctttgaaaagctccaagcctcaactgtaacctgcagc  4560

4561  aaacagataacattcctggcaagaagagacaagtcttttttaaagtttactgatgcttag  4620
4621  atctgtgggcttctagtcctctgaaagtggttgttttcctatgcacagcgagctcagaaa  4680
4681  taaaaaccccatttgaaacatccaggatgtcccaatattaccatgatttttttcccccct  4720
4721  ttttgctaatccagtccaggttggaaagaagtctcctctgtgtcagattaagccctgtct  4780
4781  cttaatgatatggacaaatgagtgtgcctaaggccatgagatgtttcctaatgcagaagg  4840
4741  aatctgttgtacgttttttgattgtactcttctatgctggaccgaattcatatgcagat  4900
4901  cgaagtgagtcctgttcttacagatggtatttgatagatactggagtttgtctgtgtt  4960
4961  atatctgtgccccttcttaaagaacaatgttgcattatgttcctttggataaattgtgat  5020
5021  ttgacaactgatttaaataaacatatttgactac(A).
```

FIG.3H

(11 of 40)

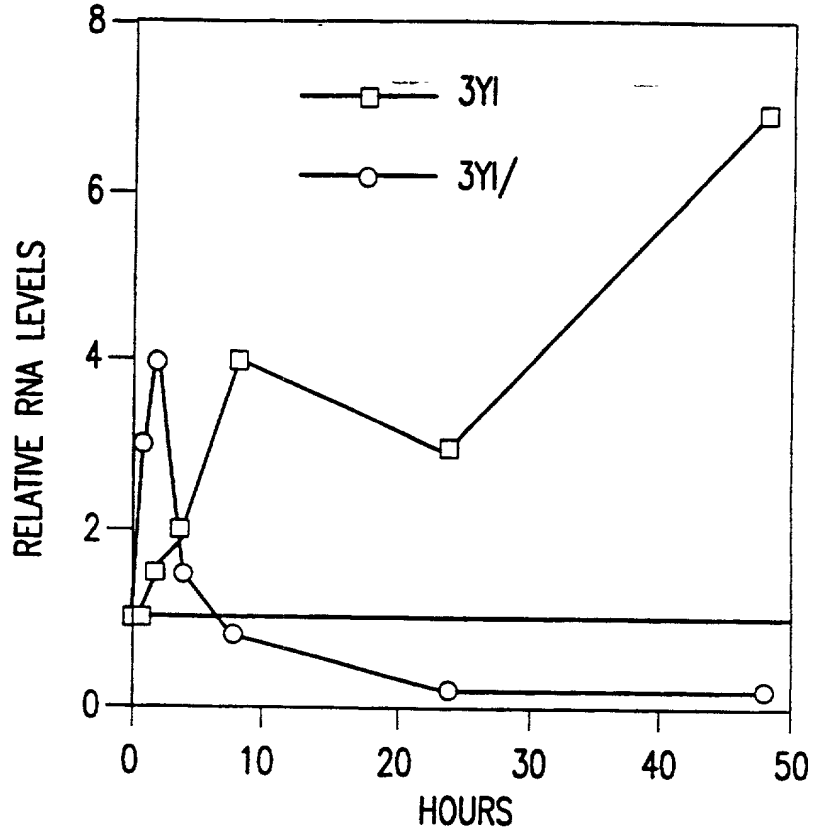

8
6
4
2
0
RELATIVE RNA LEVELS
3YI
3YI/
0
10
20
30
40
50
HOURS

FIG.4A

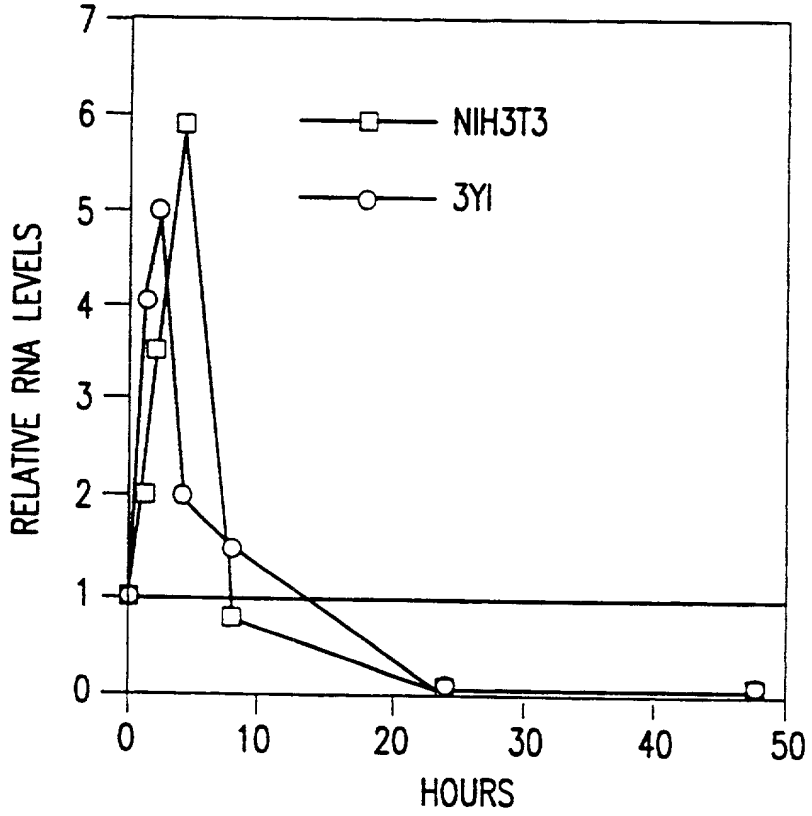

7
6
5
4
3
2
1
0
RELATIVE RNA LEVELS
NIH3T3
3YI
0
10
20
30
40
50
HOURS

FIG.4B

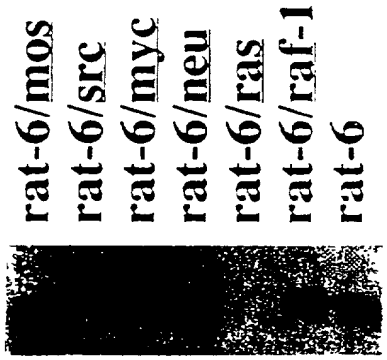


FIG.5

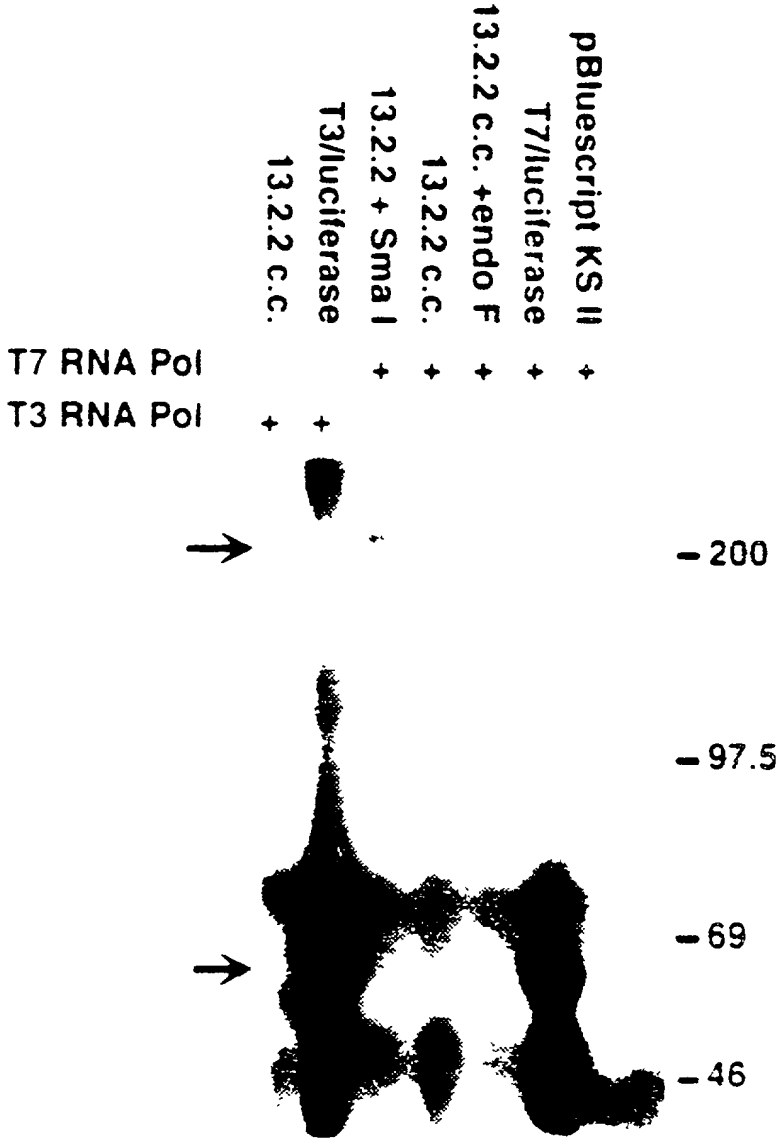

pBluescript KS II
T7/luciferase
13.2.2 c.c. +endo F
13.2.2 c.c.
13.2.2 + Sma I
T3/luciferase
13.2.2 c.c.
T7 RNA Pol
T3 RNA Pol
+
+
+
+
+
+
+
200
97.5
69
46

FIG.6

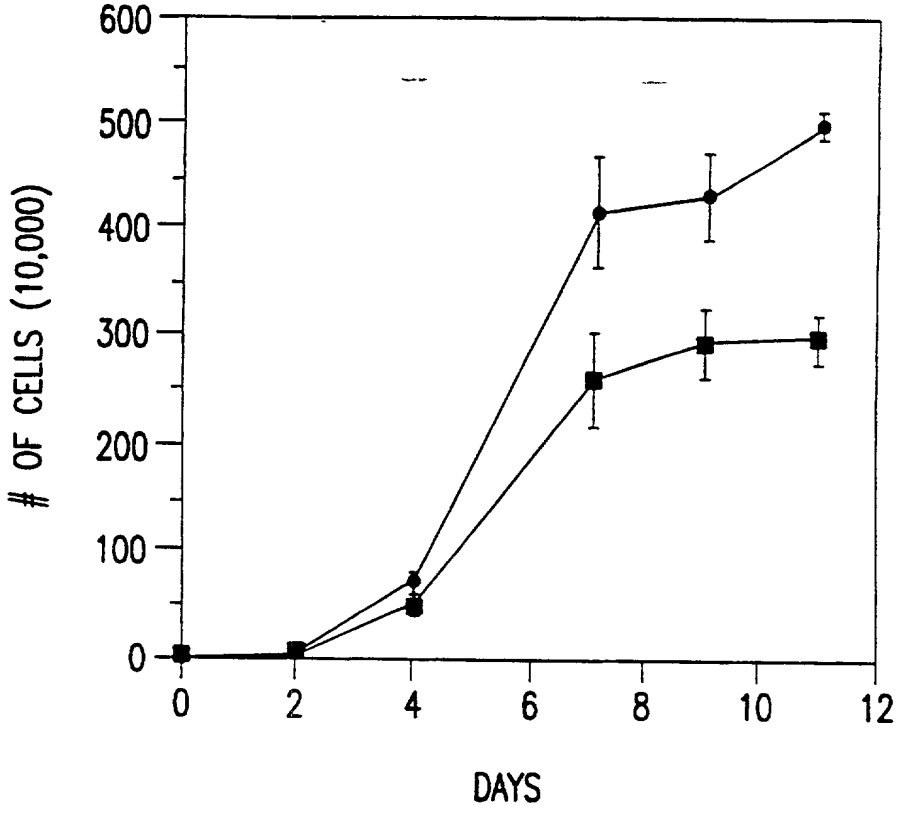

600
500
400
300
200
100
0
OF CELLS (10,000)
0
2
4
6
8
10
12
DAYS

FIG.7A

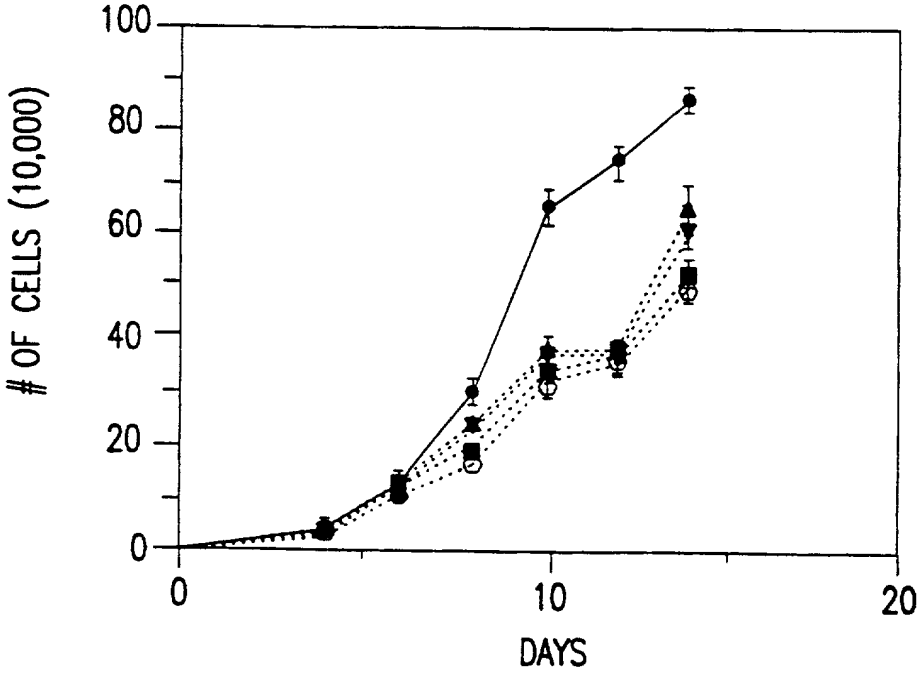

100
80
60
40
20
0
OF CELLS (10,000)
0
10
20
DAYS

FIG.7B

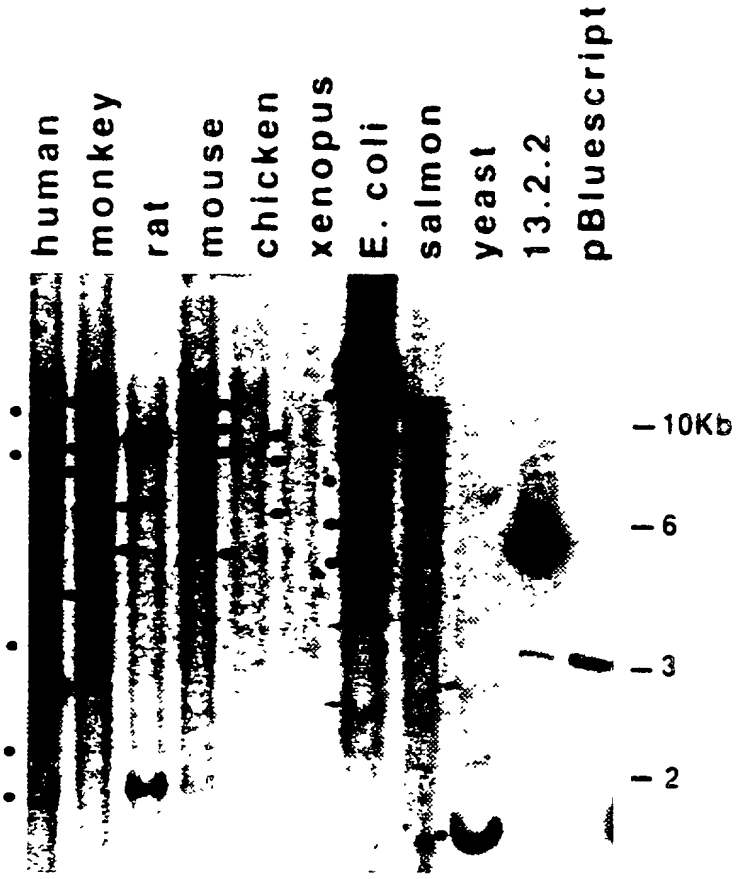

human
monkey
rat
mouse
chicken
xenopus
E. coli
salmon
yeast
13.2.2
pBluescript
10Kb
6
3
2

FIG.8

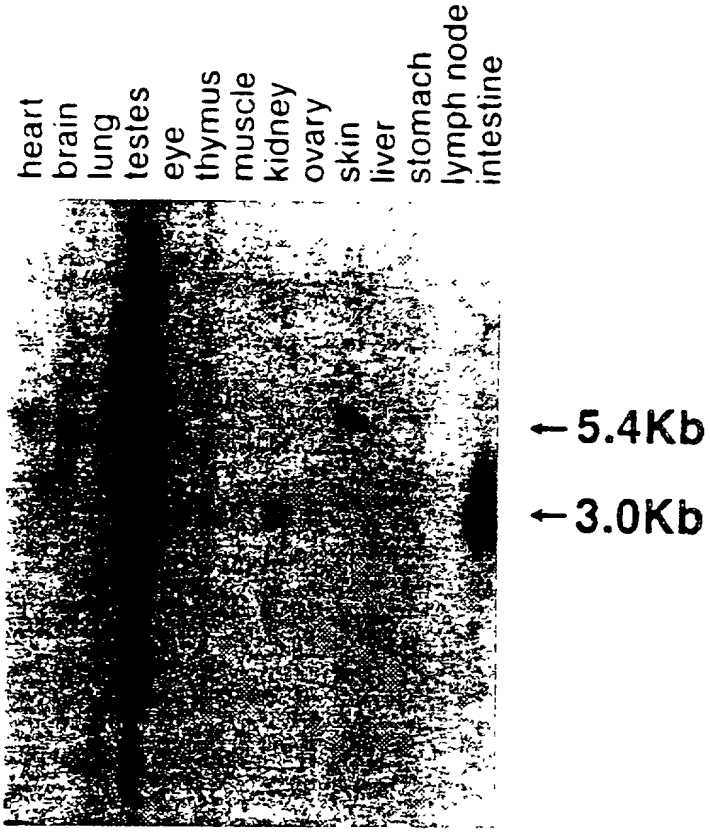

heart
brain
lung
testes
eye
thymus
muscle
kidney
ovary
skin
liver
stomach
lymph node
intestine
←5.4Kb
←3.0Kb

FIG.9

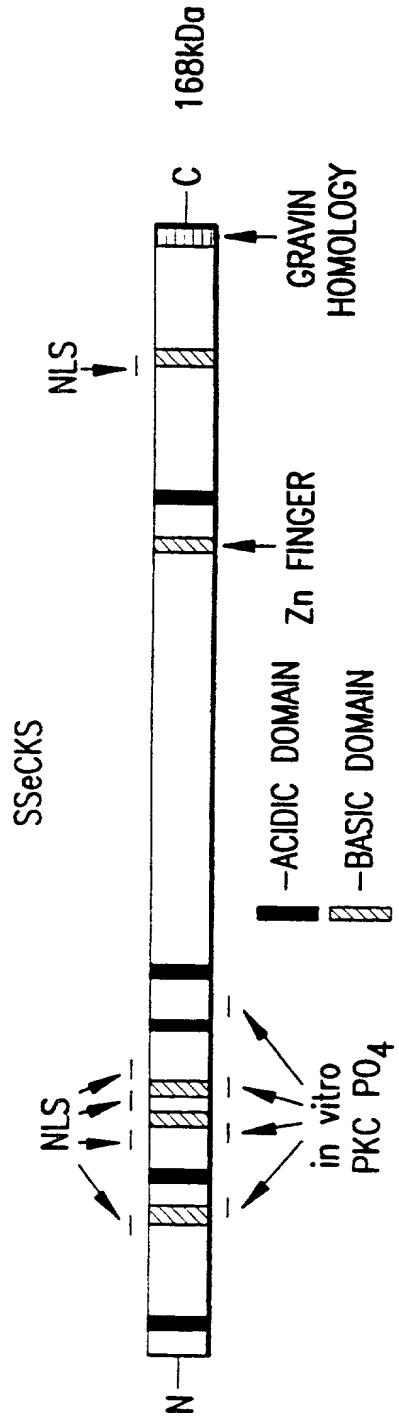

168kDa
C
GRAVIN HOMOLOGY
NLS
Zn FINGER
SSeCKS
ACIDIC DOMAIN
BASIC DOMAIN
NLS
in vitro PKC PO4
N

FIG.10

```
                9         18        27        36        45        54
5'  ATG GGC GCA GGC AGT TCC ACC GAG CAG CGG AGC CCC GAG CAG CCG GCG GGG AGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   A   G   S   S   T   E   Q   R   S   P   E   Q   P   A   G   S

               63        72        81        90        99       100
    GAC ACG CCG AGC GAG CTG GTG CTC AGT GGC CAT GGG CCC GCA GCT GAA GCC TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   P   S   E   L   V   L   S   G   H   G   P   A   A   E   A   S

              117       126       135       144       153       162
    GGA GCA GCT GGA GAC CCC GCC GAC GCG GAC CCC GCC ACC AAG CTC CCA CAG AAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   A   G   D   P   A   D   A   D   P   A   T   K   L   P   Q   K

              171       180       189       198       207       216
    AAT GGC CAG CTG TCT TCT GTC AAC GGC GTA GCT GAA CAA GGA GAT GTC CAT GTC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     N   G   Q   L   S   S   V   N   G   V   A   E   Q   G   D   V   H   V

              225       234       243       252       261       270
    CAA GAG GAA AAC CAG GAG GGG CAG GAG GAA GAA GTC GTT GAT GAG GAT GTT GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Q   E   E   N   Q   E   G   Q   E   E   E   V   V   D   E   D   V   G

              279       288       297       306       315       324
    CAG CGA GAG TCA GAA GAT GTG AGA GAA AAA GAC CGA GTT GAA GAA ATG GCG GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Q   R   E   S   E   D   V   R   E   K   D   R   V   E   E   M   A   A

              333       342       351       360       369       378
    AAC TCC ACA GCT GTT GAA GAT ATC ACA AAG GAT GGG CAG GAG GAG ACA TCA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     N   S   T   A   V   E   D   I   T   K   D   G   Q   E   E   T   S   E

              387       396       405       414       423       432
    ATA ATT GAA CAG ATC CCT GCT TCA GAA AAC AAT GTG GAA GAA ATG GTA CAG CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     I   I   E   Q   I   P   A   S   E   N   N   V   E   E   M   V   Q   P
```

FIG.11A

```
          441        450        459        468        477        486
GCT GAG TCC CAG GCT AAT GAT GTT GGC TTC AAG AAA GTA TTT AAA TTT GTT GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   S   Q   A   N   D   V   G   F   K   K   V   F   K   F   V   G

          495        504        513        522        531        540
TTT AAA TTC ACG GTG AAG AAG GAT AAA AAT GAA AAG TCA GAT ACT GTC CAA CTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   K   F   T   V   K   K   D   K   N   E   K   S   D   T   V   Q   L

          549        558        567        576        585        594
CTC ACT GTC AAG AAG GAT GAA GGC GAA GGG GCA GAA GCC TCT GTC GGA GCT GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   T   V   K   K   D   E   G   E   G   A   E   A   S   V   G   A   G

          603        612        621        630        639        648
GAC CAC CAG GAG CCC AGT GTG GAG ACT GCC GTC GGA GAG TCA GCA TCC AAA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   H   Q   E   P   S   V   E   T   A   V   G   E   S   A   S   K   E

          657        666        675        684        693        702
AGT GAG CTG AAG CAA TCC ACA GAG AAG CAA GAA GGC ACC CTG AAG CAA GAA CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   E   L   K   Q   S   T   E   K   Q   E   G   T   L   K   Q   E   Q

          711        720        729        738        747        756
AGC AGC ACA GAA ATC CCC CTT CAA GCC GAA TCT GAT CAA GCG GCT GAG GAA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   S   T   E   I   P   L   Q   A   E   S   D   Q   A   A   E   E   E

          765        774        783        792        801        810
GCC AAA GAT GAA GGA GAA GAA AAA CAA GAG AAA GAG CCC ACC AAG TCC CCA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   K   D   E   G   E   E   K   Q   E   K   E   P   T   K   S   P   E

          819        828        837        846        855        864
TCC CCG AGC AGC CCA GTC AAC AGT GAG ACA ACA TCT TCC TTC AAG AAG TTC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   P   S   S   P   V   N   S   E   T   T   S   S   F   K   K   F   F
```

FIG.11B

```
          873         882         891         900         909         918
ACT CAC GGT TGG GCC GGC TGG CGC AAG AAG ACC AGC TTC AAG AAA TCA AAA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   H   G   W   A   G   W   R   K   K   T   S   F   K   K   S   K   E

          927         936         945         954         963         972
GAT GAT CTG GAA ACT GCC GAG AAG AGA AAG GAG CAA GAG GCA GAA AAA GTA GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   D   L   E   T   A   E   K   R   K   E   Q   E   A   E   K   V   D

          981         990         999        1008        1017        1026
GAG GAA GAA AAG GAA AAG ACA GAG CCA GCC TCG GAG GAG CAG GAG CCG GCA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   E   K   E   K   T   E   P   A   S   E   E   Q   E   P   A   E

         1035        1044        1053        1062        1071        1080
GAC ACA GAC CAG GCC AGG TTG TCA GCA GAC TAC GAG AAG GTG GAG CTG CCT TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   T   D   Q   A   R   L   S   A   D   Y   E   K   V   E   L   P   L

         1089        1098        1107        1116        1125        1134
GAA GAC CAG GTT GGT GAC CTG GAG GCA TCG TCA GAG GAG AAG TGT GCT CCT TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   Q   V   G   D   L   E   A   S   S   E   E   K   C   A   P   L

         1143        1152        1161        1170        1179        1188
GCA ACG GAA GTG TTT GAT GAG AAG ATG GAA GCC CAC CAA GAA GTT GTT GCA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   T   E   V   F   D   E   K   M   E   A   H   Q   E   V   V   A   E

         1197        1206        1215        1224        1233        1242
GTC CAC GTG AGC ACC GTG GAG AAG ACA GAG GAG GAG CAG GGA GGA GGA GGA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   H   V   S   T   V   E   K   T   E   E   E   Q   G   G   G   G   E

         1251        1260        1269        1278        1287        1296
GCT GAA GGG GGC GTG GTG GTA GAA GGA ACA GGA GAA TCC TTG CCC CCT GAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   G   G   V   V   V   E   G   T   G   E   S   L   P   P   E   K
```

FIG.11C

```
      1305       1314       1323       1332       1341       1350
CTG GCT GAG CCC CAG GAG GTC CCC CAG GAA GCT GAG CCT GCT GAG GAG CTG ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   A   E   P   Q   E   V   P   Q   E   A   E   P   A   E   E   L   M

      1359       1368       1377       1386       1395       1404
AAG AGC AGA GAG ATG TGT GTC TCT GGA GGA GAC CAC ACT CAA CTG ACA GAC CTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   S   R   E   M   C   V   S   G   G   D   H   T   Q   L   T   D   L

      1413       1422       1431       1440       1449       1458
AGT CCT GAA GAG AAG ACG CTG CCC AAA CAC CCA GAA GGC ATT GTC AGT GAG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   P   E   E   K   T   L   P   K   H   P   E   G   I   V   S   E   V

      1467       1476       1485       1494       1503       1512
GAG ATG CTG TCC TCT CAG GAA AGA ATC AAG GTA CAG GGA AGT CCC TTG AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   M   L   S   S   Q   E   R   I   K   V   Q   G   S   P   L   K   K

      1521       1530       1539       1548       1557       1566
CTC TTC AGT AGC TCA GGC TTA AAG AAG CTG TCT GGG AAG AAG CAG AAG GGG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   F   S   S   S   G   L   K   K   L   S   G   K   K   Q   K   G   K

      1575       1584       1593       1602       1611       1620
CGA GGA GGT GGG GGA GAC GAA GAG CCT GGA GAA TAC CAA CAC ATT CAC ACC GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   G   G   G   G   D   E   E   P   G   E   Y   Q   H   I   H   T   E

      1629       1638       1647       1656       1665       1674
TCC CCA GAG AGT GCT GAT GAG CAG AAG GGA GAG AGC TCT GCG TCG TCC CCC GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   P   E   S   A   D   E   Q   K   G   E   S   S   A   S   S   P   E

      1683       1692       1701       1710       1719       1728
GAG CCT GAG GAG ACC ACG TGT CTG GAG AAA GGG CCG CTG GAA GCA CCC CAG GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   P   E   E   T   T   C   L   E   K   G   P   L   E   A   P   Q   D
```

FIG.11D

```
      1737       1746       1755       1764       1773       1782
GGG GAA GCT GAG GAA GGA ACT ACT TCC GAT GGA GAG AAG AAG AGA GAA GGG ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   E   A   E   E   G   T   T   S   D   G   E   K   K   R   E   G   I

      1791       1800       1809       1818       1827       1836
ACT CCC TGG GCA TCC TTC AAA AAG ATG GTG ACA CCC AAG AAA CGG GTC CGA AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   P   W   A   S   F   K   K   M   V   T   P   K   K   R   V   R   R

      1845       1854       1863       1872       1881       1890
CCT TCT GAG AGT GAC AAG GAG GAA GAG CTG GAG AAG GTC AAG AGC GCC ACC TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   S   F   S   D   K   E   E   E   L   E   K   V   K   S   A   T   L

      1899       1908       1917       1926       1935       1944
TCC TCC ACT GAT AGC ACA GTG TCA GAA ATG CAA GAT GAA GTC AAA ACT GTT GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   S   T   D   S   T   V   S   E   M   Q   D   E   V   K   T   V   G

      1953       1962       1971       1980       1589       1998
GAG GAA CAA AAG CCA GAG GAA CCA AAG CGT AGG GTG GAT ACT TCA GTG TCT TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   Q   K   P   E   E   P   K   R   R   V   D   T   S   V   S   W

      2007       2016       2025       2034       2043       2052
GAA GCA CTG ATT TGT GTC GGA TCA TCC AAG AAG AGA GCA AGG AAG GCA TCC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   A   L   I   C   V   G   S   S   K   K   R   A   R   K   A   S   S

      2061       2070       2079       2088       2097       2106
TCA GAT GAT GAA GGA GGG CCA AGG ACA CTG GGA GGG GAC AGT CAC AGA GCA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   D   D   E   G   G   P   R   T   L   G   G   D   S   H   R   A   E

      2115       2124       2133       2142       2151       2160
GAG GCC AGC AAA GAC AAA GAA GCC GGA ACA GAC GCT GTT CCT GCC AGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   A   S   K   D   K   E   A   G   T   D   A   V   P   A   S   T   Q
```

FIG.11E

```
      2169       2178       2187       2196       2205       2114
GAG CAG GAC CAA GCG CAA GGA AGT ICC TCA CCC GAG CCA GCG GGA AGC CTT TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   Q   D   Q   A   Q   G   S   S   S   P   E   P   A   G   S   P   S

      2223       2232       2241       2250       2259       2268
GAA GGG GAA GGT GTC TCC ACT TGG GAG TCA TTT AAA AGA TTA GTC ACT CCA AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   E   G   V   S   T   W   E   S   F   K   R   L   V   T   P   R

      2277       2286       2295       2304       2313       2322
AAA AAA TCC AAG TCA AAA CTG GAA GAG AAA GCC GAA GAC TCT AGT GTA GAG CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   K   S   K   S   K   L   E   E   K   A   E   D   S   S   V   E   Q

      2331       2340       2349       2358       2367       2376
TTG TCC ACT GAG ATC GAA CCG AGT AGA GAA GAA TCT TGG GTT TCC ATT AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   S   T   E   I   E   P   S   R   E   E   S   W   V   S   I   K   K

      2385       2394       2403       2412       2421       2430
TTC ATC CCC GGA CGG CGG AAG AAA AGG GCA GAC GGG AAG CAA GAA CAA GCC ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   I   P   G   R   R   K   K   R   A   D   G   K   Q   E   Q   A   T

      2439       2448       2457       2466       2475       2484
GTG GAA GAC TCA GGG CCA GTG GAG ATA AAT GAG GAC GAC CCT AAT GTC CCA GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   D   S   G   P   V   E   I   N   E   D   D   P   N   V   P   A

      2493       2502       2511       2520       2529       2538
GTC GTG CCT CTG TCT GAG TAT AAT GCA GTG GAG AGG GAG AAG ATG GAA GCC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   V   P   L   S   E   Y   N   A   V   E   R   E   K   M   E   A   Q

      2547       2556       2565       2574       2583       2592
GGG AAT ACG GAG CTG CCC CAG CTG CTG GGG GCT GTG TAC GTG TCC GAG GAG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   N   T   E   L   P   Q   L   L   G   A   V   Y   V   S   E   E   L
```

FIG.11F

```
      2601       2610       2619       2628       2637       2646
AGT AAG ACT CTG GTC CAC ACT GTG AGT GTC GCA GTC ATT GAT GGG ACC AGG GCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   K   T   L   V   H   T   V   S   V   A   V   I   D   G   T   R   A

      2655       2664       2673       2682       2691       2700
GTC ACC AGT GTC GAA GAG CGG TCT CCT TCG TGG ATA TCC GCT TCC GTA ACA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   T   S   V   E   E   R   S   P   S   W   I   S   A   S   V   T   E

      2790       2718       2727       2736       2745       2754
CCT CTT GAA CAC ACA GCG GGA GAA GCC ATG CCA CCT GTT GAA GAG GTC ACT GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   L   E   H   T   A   G   E   A   M   P   P   V   E   E   V   T   E

      2763       2772       2781       2790       2799       2808
AAA GAC ATC ATT GCA GAA GAA ACT CCT GTG CTC ACC CAG ACG TTA CCA GAG GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   D   I   I   A   E   E   T   P   V   L   T   Q   T   L   P   E   G

      2817       2826       2835       2844       2853       2862
AAA GAT GCC CAT GAC GAC ATG GTC ACC AGT GAA GTG GAT TTC ACC TCA GAA GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   D   A   H   D   D   M   V   T   S   E   V   D   F   T   S   E   A

      2871       2880       2889       2898       2907       2916
GTG ACA GCC ACA GAG ACC TCA GAG GCT CTC CGT ACT GAA GAA GTT ACC GAA GCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   T   A   T   E   T   S   E   A   L   R   T   E   E   V   T   E   A

      2925       2934       2943       2952       2961       2970
TCG GGG GCC GAA GAG ACC ACA GAC ATG GTG TCC GCA GTT TCC CAG CTG ACT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   A   E   E   T   T   D   M   V   S   A   V   S   Q   L   T   D

      2979       2988       2997       3006       3015       3024
TCC CCA GAC ACC ACA GAG GAA GCC ACC CCA GTT CAG GAG GTA GAG AGT GGT GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   P   D   T   T   E   E   A   T   P   V   Q   E   V   E   S   G   V
```

FIG.11G

```
      3033        3042        3051        3060        3069        3078
CTA GAT ACA GAA GAA GAG GAG CGC CAG ACG CAG GCC ATC CTC CAA GCC GTT GCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   D   T   E   E   E   E   R   Q   T   Q   A   I   L   Q   A   V   A

      3087        3096        3105        3114        3123        3132
GAC AAG GTG AAA GAG GAG TCC CAG GTG CCT GCA ACC CAG ACT GTG CAG AGA ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   V   K   E   E   S   Q   V   P   A   T   Q   T   V   Q   R   T

      3141        3150        3159        3168        3177        3186
GGG TCA AAA GCA CTG GAG AAG GTT GAG GAG GTA GAG GAG GAC TCC GAA GTG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   S   K   A   L   E   K   V   E   E   V   E   E   D   S   E   V   L

      3195        3204        3213        3222        3231        3240
GCT TCG GAG AAA GAG AAG GAC GTT ATG CCG AAA GGA CCC GTG CAG GAA GCT GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   S   E   K   E   K   D   V   M   P   K   G   P   V   Q   E   A   G

      3195        3258        3267        3276        3285        3294
GCT GAG CAT CTT GCA CAG GGC TCT GAG ACT GGA CAG GCT ACT CCA GAG AGC CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   H   L   A   Q   G   S   E   T   G   Q   A   T   P   E   S   L

      3303        3312        3321        3330        3339        3348
GAA GTT CCT GAA GTC ACG GCA GAT GTA GAC CAT GTC GCC ACG TGC CAG GTT ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   V   P   E   V   T   A   D   V   D   H   V   A   T   C   Q   V   I

      3357        3366        3375        3384        3393        3402
AAG CTC CAG CAG CTG ATG GAA CAG GCC GTG GCC CCT GAG TCA TCC GAA ACC TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   L   Q   Q   L   M   E   Q   A   V   A   P   E   S   S   E   T   L

      3411        3420        3429        3438        3447        3456
ACA GAC AGT GAG ACA AAT GGA AGC ACT CCC TTA GCA GAT TCA GAC ACT GCA GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   D   S   E   T   N   G   S   T   P   L   A   D   S   D   T   A   D
```

FIG.11H

```
      3465       3474       3483       3492       3501       3510
GGG ACA CAG CAA GAT GAA ACC ATT GAC AGC CAG GAC AGT AAA GCC ACT GCA GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   T   Q   Q   D   E   T   I   D   S   Q   D   S   K   A   T   A   A

      3519       3528       3537       3546       3555       3564
GTC AGG CAG TCA CAG GTC ACA GAA GAA GAG GCG GCT ACT GCT CAG AAA GAG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   R   Q   S   Q   V   T   E   E   E   A   A   T   A   Q   K   E   E

      3573       3582       3591       3600       3609       3618
CCT TCG ACA CTA CCT AAT AAT GTT CCA GCC CAG GAA GAA CAT GGG GAA GAA CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   S   T   L   P   N   N   V   P   A   Q   E   E   H   G   E   E   P

      3627       3636       3645       3654       3663       3672
GGA AGA GAT GTT CTT GAA CCT ACA CAG CAA GAG CTT ACT GCT GCA GCC GTG CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   R   D   V   L   E   P   T   Q   Q   E   L   T   A   A   A   V   P

      3681       3690       3699       3708       3717       3726
GTT CTG GCA AAG ACT GAG GTG GGT CAA GAG GGT GAG GTT GAC TGG TTG GAT GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   A   K   T   E   V   G   Q   E   G   E   V   D   W   L   D   G

      3735       3744       3753       3762       3771       3780
GAA AAA GTC AAA GAA GAA CAG GAG GTG TTT GTA CAC TCT GGA CCC AAC AGT CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   K   V   K   E   E   Q   E   V   F   V   H   S   G   P   N   S   Q

      3789       3798       3807       3816       3825       3834
AAG GCT GCT GAT GTG ACA TAT GAC AGT GAA GTG ATG GGA GTG GCC GGG TGT CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   A   A   D   V   T   Y   D   S   E   V   M   G   V   A   G   C   Q

      3843       3852       3861       3870       3879       3888
GAA AAG GAG AGT ACT GAA GTG CAG AGT CTT AGC CTG GAG GAG GGA GAG ATG GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   K   E   S   T   E   V   Q   S   L   S   L   E   E   G   E   M   E
```

FIG.11I

```
      3897        3906        3915        3924        3933        3942
ACT GAC GTT GAA AAG GAG AAA AGG GAG ACA AAG CCA GAG CAA GTG AGT GAA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   D   V   E   K   E   K   R   E   T   K   P   E   Q   V   S   E   E

      3951        3960        3969        3978        3987        3996
GGT GAG CAG GAA ACA GCC GCT CCT GAG CAT GAA GGA ACC TAC GGG AAG CCA GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   E   Q   E   T   A   A   P   E   H   E   G   T   Y   G   K   P   V

      4005        4014        4023        4032        4041        4050
CTG ACA CTT GAC ATG CCC AGC TCA GAG AGG GGG AAG GCA CTG GGA AGC CTT GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   T   L   D   M   P   S   S   E   R   G   K   A   L   G   S   L   G

      4059        4068        4077        4086        4095        4104
GGA AGC CCT TCT CTC CCA GAC CAA GAC AAA GCA GGT TGC ATA GAG GTT CAA GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   S   P   S   L   P   D   Q   D   K   A   G   C   I   E   V   Q   V

      4113        4122        4131        4140        4149        4158
CAA AGC CTG GAC ACA ACA GTC ACT CAA ACA GCA GAA GCT GTG GAA AAG GTC ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   S   L   D   T   T   V   T   Q   T   A   E   A   V   E   K   V   I

      4167        4176        4185        4194        4203        4212
GAA ACG GTT GTG ATT TCA GAG ACA GGT GAA AGT CCA GAG TGT GTA GGT GAC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   T   V   V   I   S   E   T   G   E   S   P   E   C   V   G   A   H

      4221        4230        4239        4248        4257        4266
TTA TTA CCA GCT GAG AAG TCC TCT GCA ACG GGT GGC CAC TGG ACT CTT CAG CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   L   P   A   E   K   S   S   A   T   G   G   H   W   T   L   Q   H

      4275        4284        4293        4902        4311        4320
GCA GAG GAC ACG GTA CCC CTG GGG CCT GAG TCT CAG GCA GAA TCC ATC CCA ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   D   T   V   P   L   G   P   E   S   Q   A   E   S   I   P   I
```

FIG.11J

```
      4329        4338        4347        4356        4365        4374
ATA GTA ACT CCT GCT CCT GAA AGC ACC CTA CAT CCT GAC CTA CAA GGA GAA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   T   P   A   P   E   S   T   L   H   P   D   L   Q   G   E   I

      4383        4392        4401        4410        4419        4428
AGC GCA TCC CAG AGA GAG CGA TCA GAG GAA GAG GAC AAG CCA GAT GCT GGT CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   A   S   Q   R   E   R   S   E   E   E   D   K   P   D   A   G   P

      4437        4446        4455        4464        4473        4482
GAT GCT GAC GGC AAG GAG AGT ACA GCA ATC GAA AAA GTC CTC AAG GCT GAA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   A   D   G   K   E   S   T   A   I   E   K   V   L   K   A   E   P

      4491        4500        4509        4518        4527        4536
GAG ATC CTG GAA CTT GAG AGT AAG AGC AAC AAG ATT GTG CTG AAC GTC ATT CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   I   L   E   L   E   S   K   S   N   K   I   V   L   N   V   I   Q

      4545        4554        4563        4572        4581        4590
ACA GCC GTT GAC CAG TTC GCA CGT ACA GAA ACA GCC CCC GAA ACT CAT GCT TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   A   V   D   Q   F   A   R   T   E   T   A   P   E   T   H   A   Y

      4599        4608        4617        4626        4635        4644
GAT TCA CAG ACC CAG GTT CCT GCA TGC AGG CTT GAC AGC AGG GAG CCC AAC AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   S   Q   T   Q   V   P   A   C   R   L   D   S   R   E   P   N   R

      4653        4662        4671        4680        4689        4698
TGC TGG ACA AAA ATG AAA GAT GCC AAG ATG AAA CAC CCA GTG CCG CAG CCC AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   W   T   K   M   K   D   A   K   M   K   H   P   V   P   Q   P   R

      4707        4716        4725        4734        4743        4752
GAG GAC TTG CAA GTC CTG ACC GTT CTG GAG GCA TGG GCT CAG CCT CGG AAA TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   L   Q   V   L   T   V   L   E   A   W   A   Q   P   R   K   C
```

FIG.11K

```
      4761        4770        4779        4788        4797        4806
TTG CCG CGC TTG CAG TTG AAA GCG CCG GTG TCA AAG TAA GCA TTG AGA AGC TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   P   R   L   Q   L   K   A   P   V   S   K   *

      4815        4824        4833        4842        4851        4860
CTC CTC AAC CCA AAG ATC CAA AAG GAG CAT GCT GCT GAT GGC CCT CAG CTC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      4869        4878        4887        4896        4905        4914
AGC TTA GCC CAG GCA GAG GCC AGT GCC TCT GGA AAC CTA ACC AAA GAA TCC CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      4923        4932        4941        4950        4959        4968
GAC ACC ACC GGA CCA AAG CTA ACC GAG GAG GGC GAT CCC CCA AAA GTT CAG GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      4977        4986        4995        5004        5013        5022
CAG GAA GAA GAA ATG TCT ACC AAG TCA GTC AAA GAG AAC AAG GCC CAG GCA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      5031        5040        5049        5058        5067        5076
GAG GAC CTG CAG GAG CCA AAG GGA GAC CTG GCA GAA TCC TCC GAT GTT AGT TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      5085        5094        5103        5112        5121        5130
TCA TTG TAC ATC TGT AAG ACC AGA ATG TGA AAA CAA GTC ACA GAA CAA GAT GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      5139        5148        5157        5166        5175        5184
GCT GTT GGG ACC TTG AGA CCA AGA TTT CAG AGC CCA TGA CAT CCA GAG AGC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      5193
GCC GTC CAA TGA TTT C 3'
--- --- --- --- --- -
```

FIG.11L

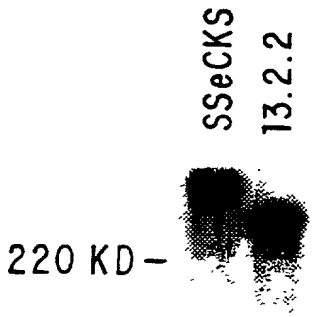


FIG. 12

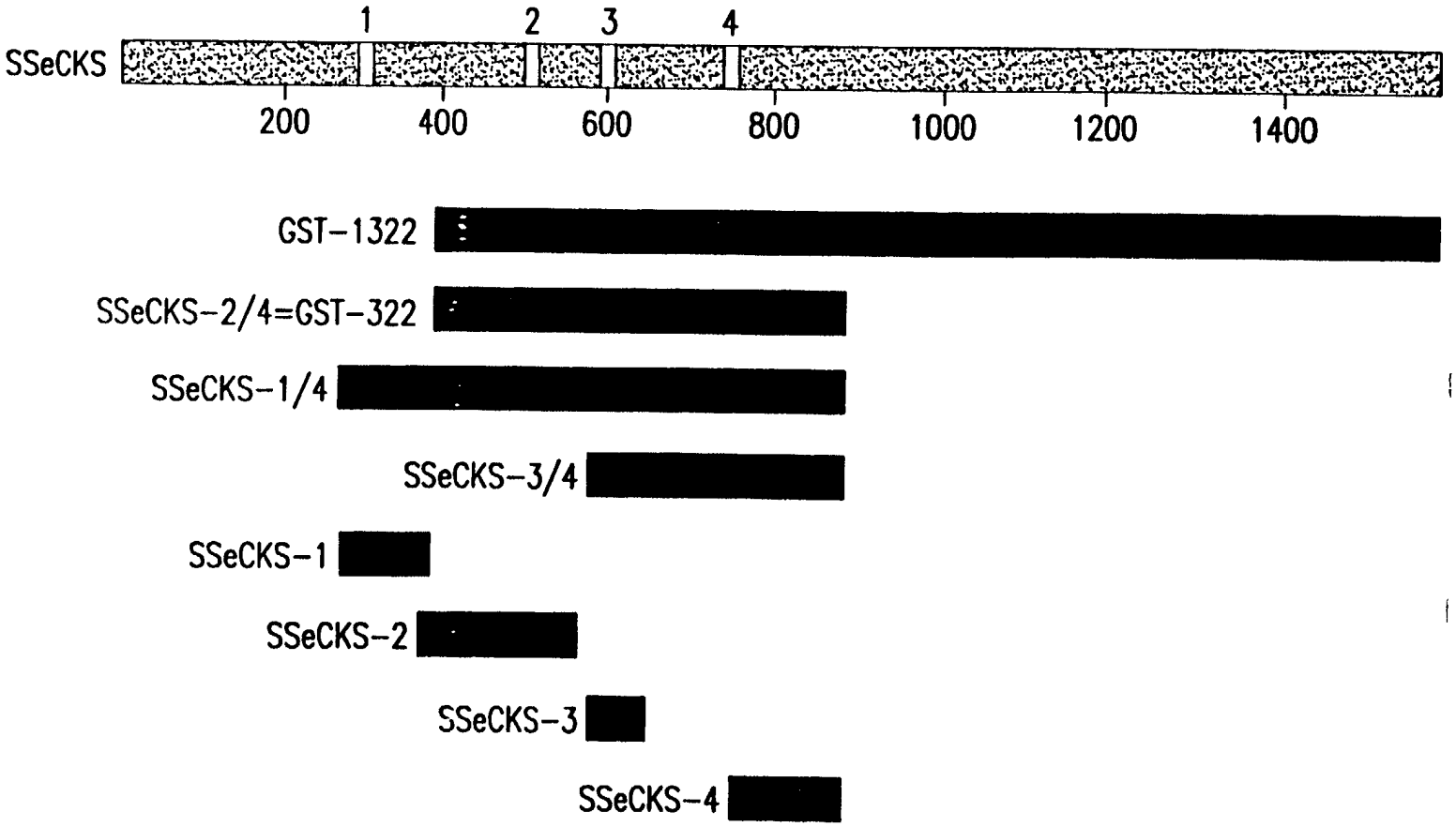


FIG.13A

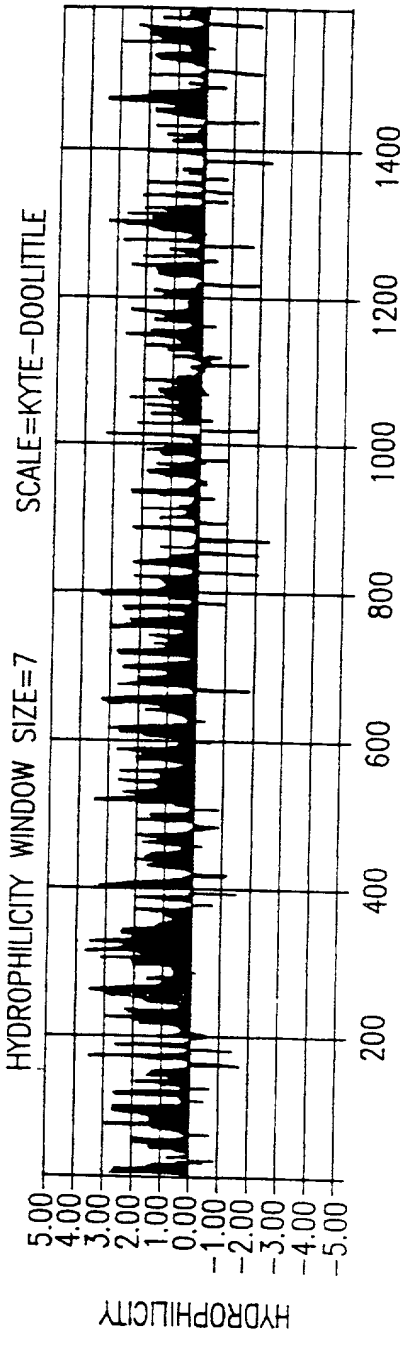


FIG.13B

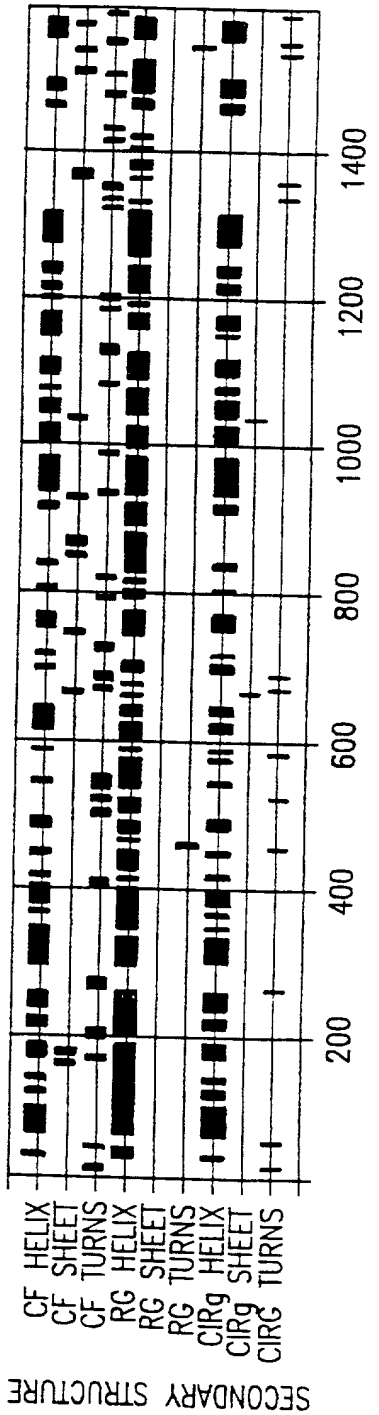


FIG.13C

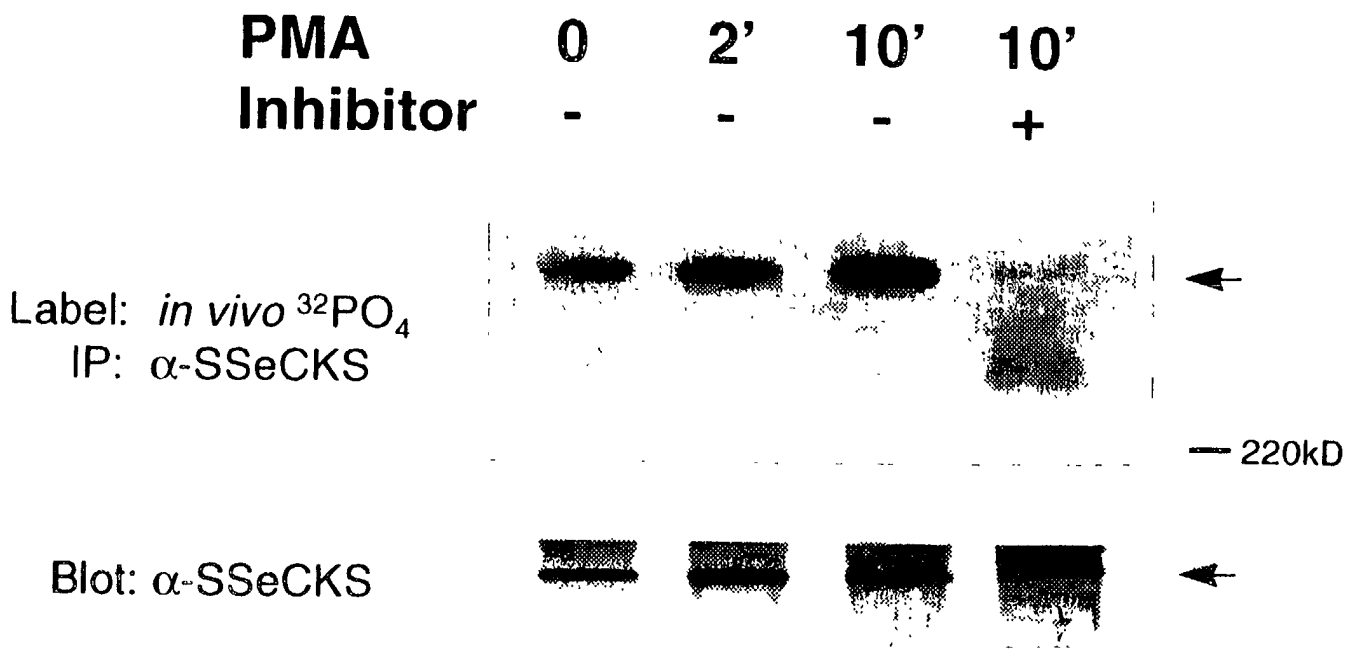


FIG.14

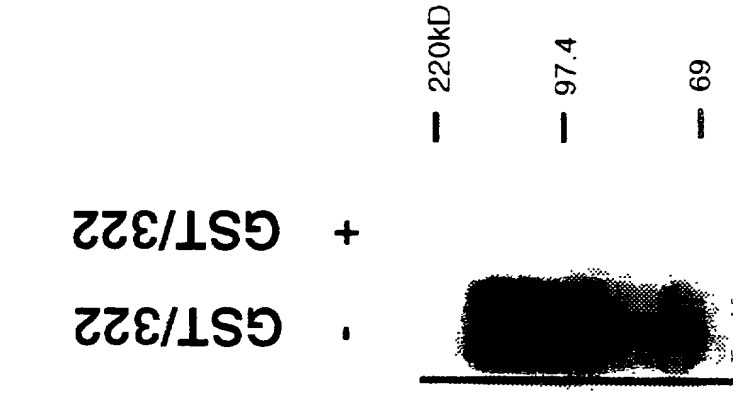


FIG. 15B

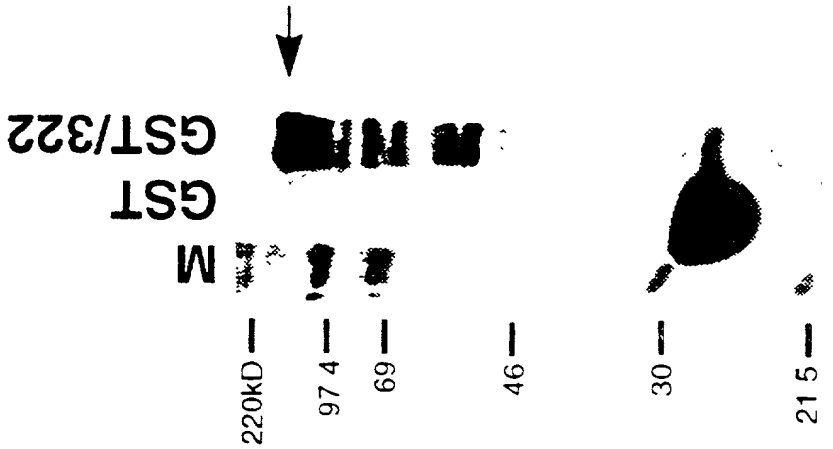


FIG. 15A

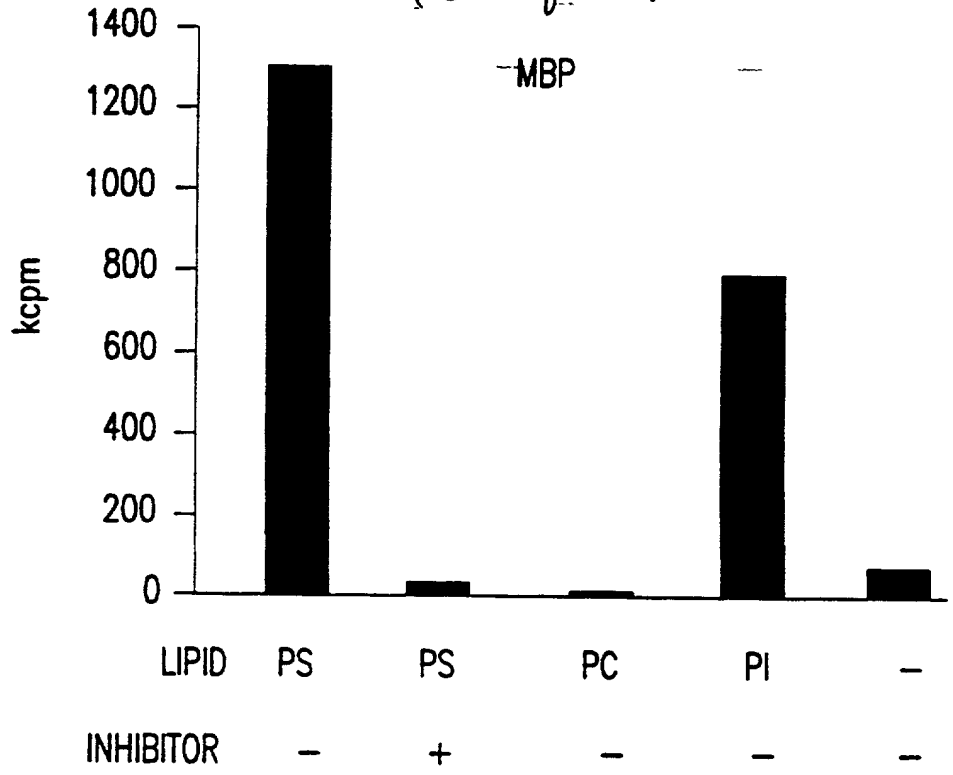


FIG.16A

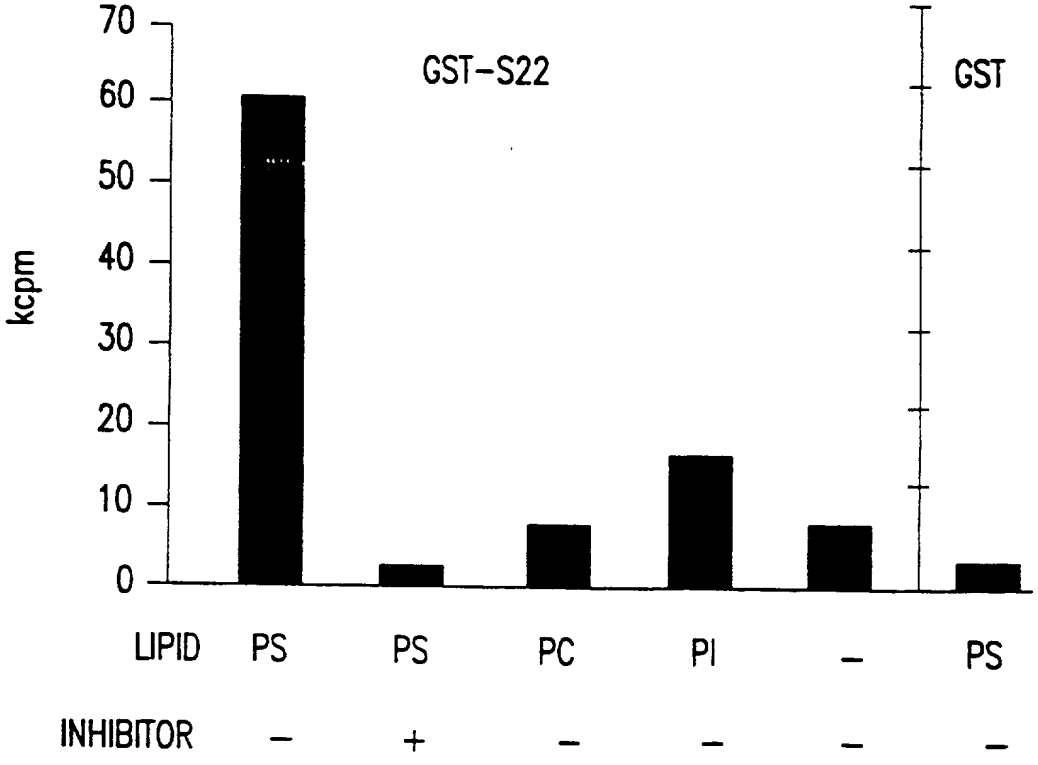


FIG.16B

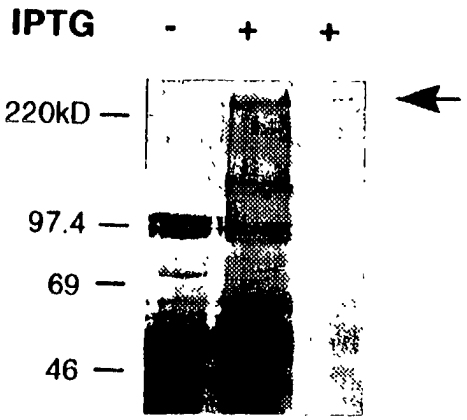


FIG.17A

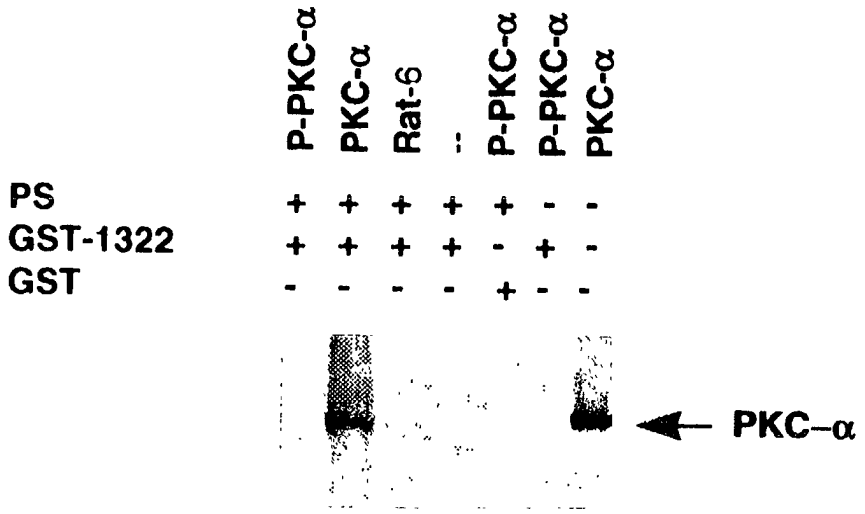


FIG.17B

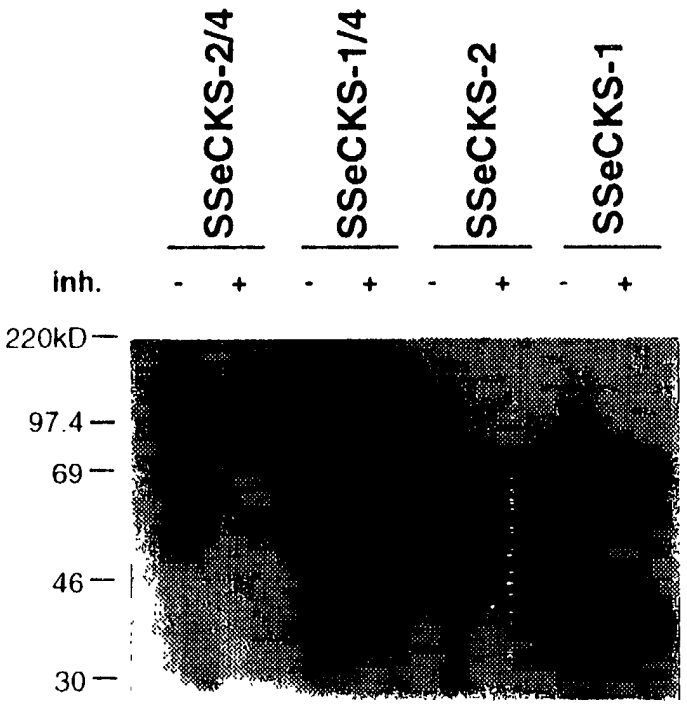


FIG.18A

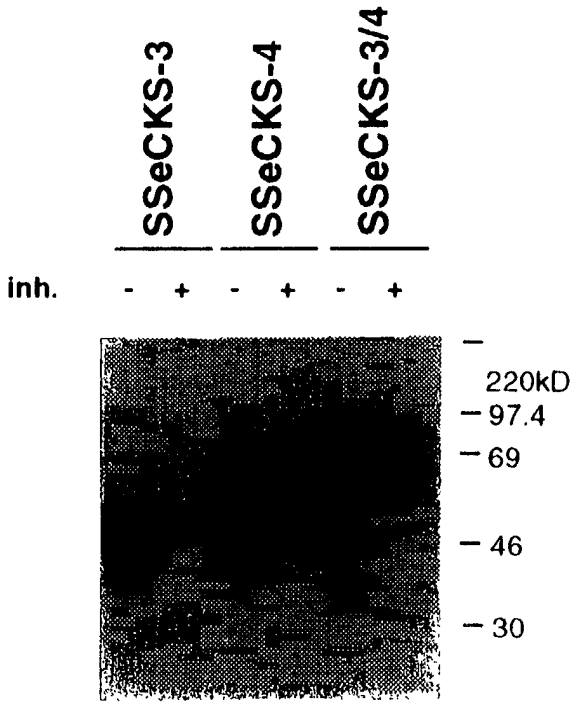
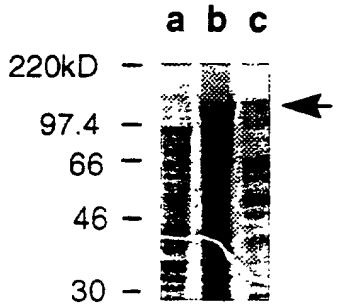


FIG.18B

(38 of 90)

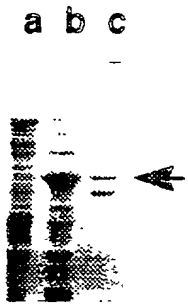


SSeCKS-2/4

FIG.18C

SSeCKS-1/4

FIG.18D

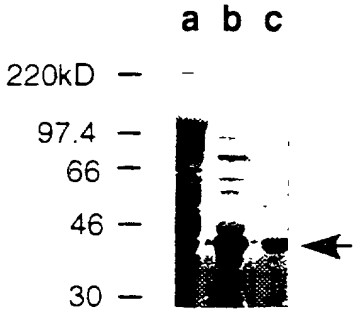


SSeCKS-2

FIG.18E

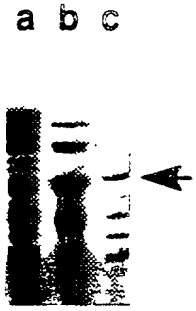
SSeCKS-1

FIG.18F



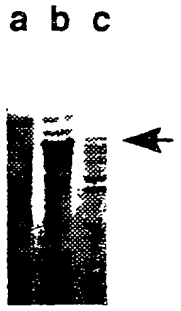
SSeCKS-3

FIG.18G



SSeCKS-4

FIG.18H



SSeCKS-3/4

FIG.18I

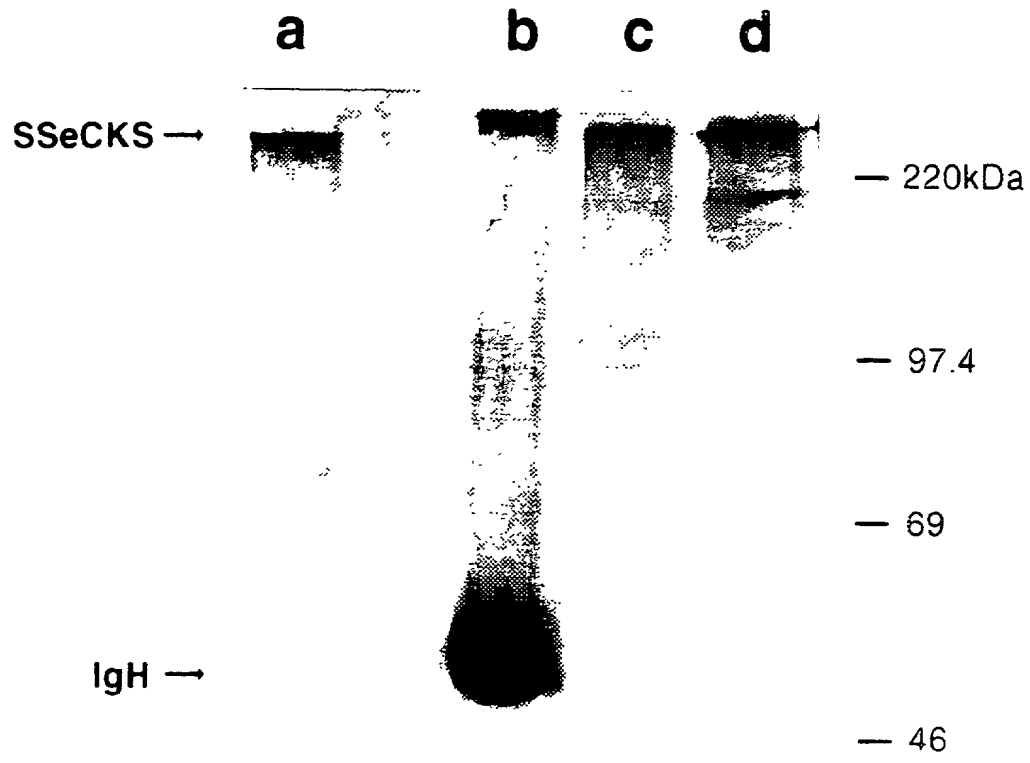


FIG.19

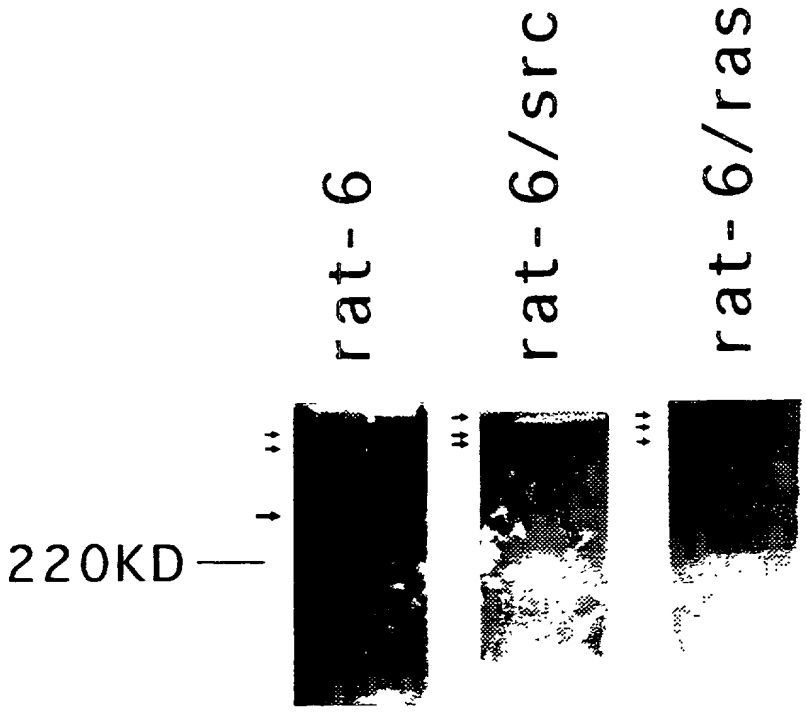


FIG.20

FIG.21A

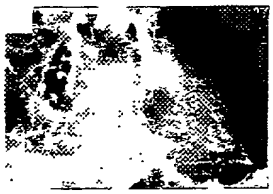


FIG.21B

FIG.21C

FIG.21D

FIG.21E

FIG.21F

FIG.21G

FIG.21H

FIG.21I

FIG.21J

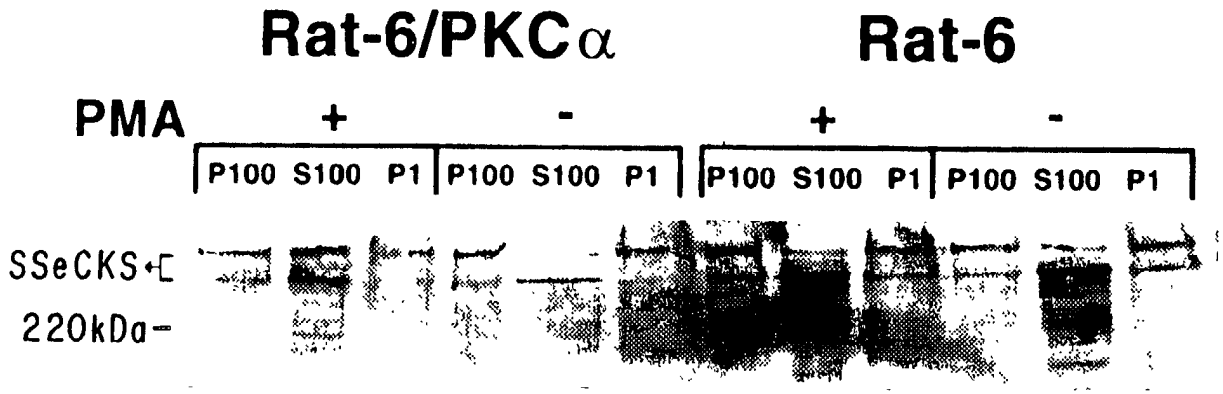


FIG.22

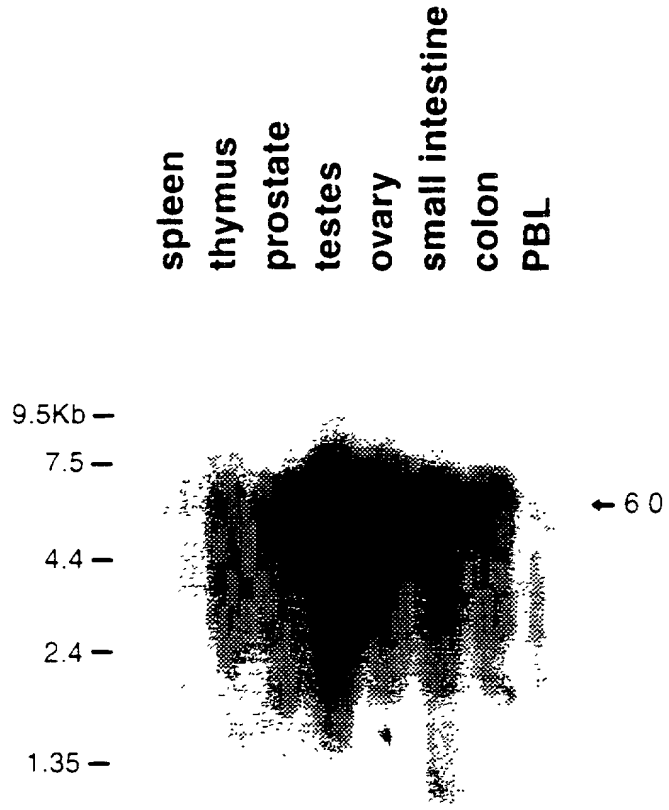


FIG.23A

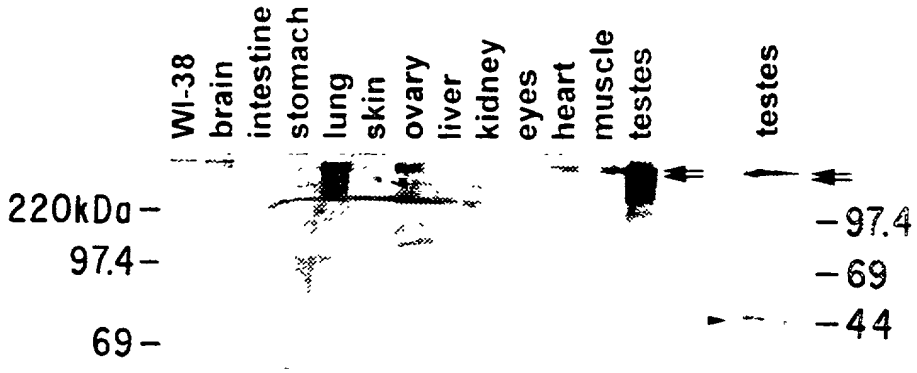


FIG.23B

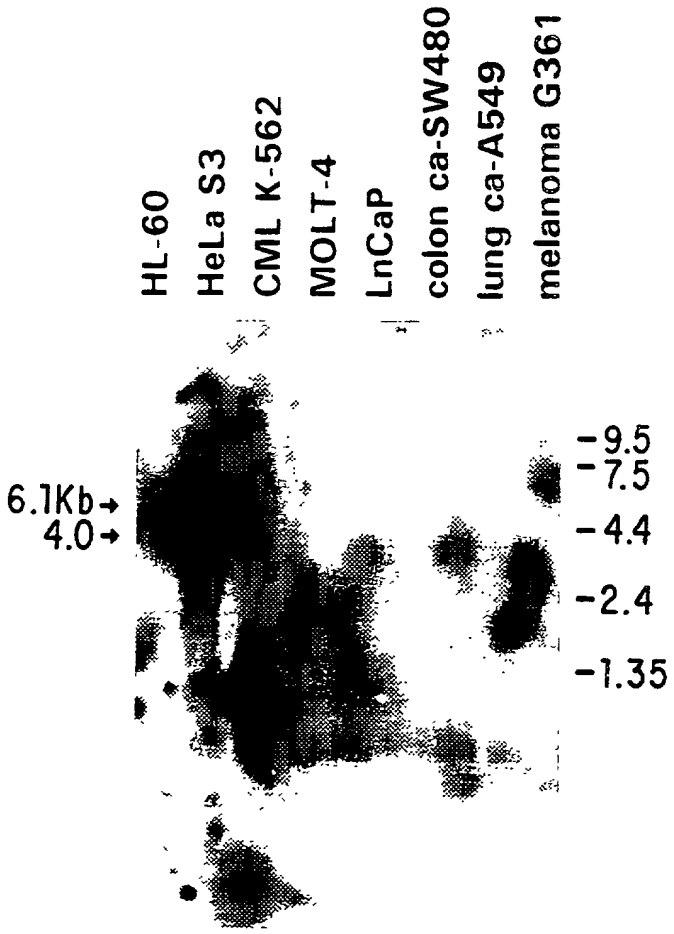

HL-60
HeLa S3
CML K-562
MOLT-4
LnCaP
colon ca-SW480
lung ca-A549
melanoma G361
6.1Kb
4.0
9.5
7.5
4.4
2.4
1.35

FIG.24

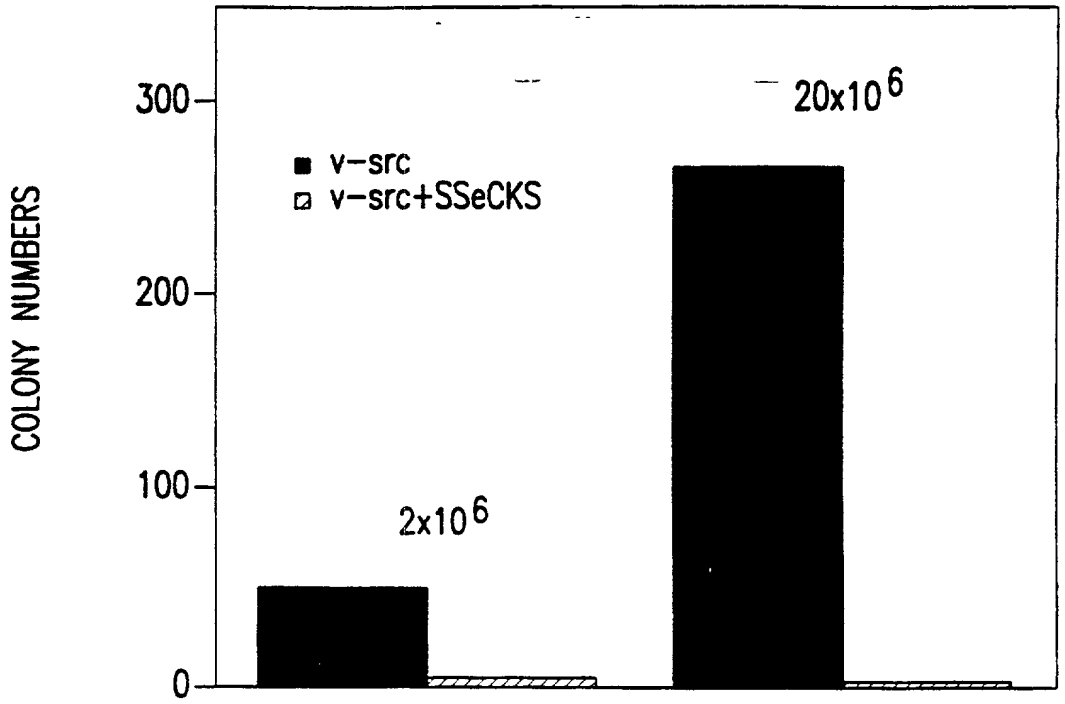


FIG.25A

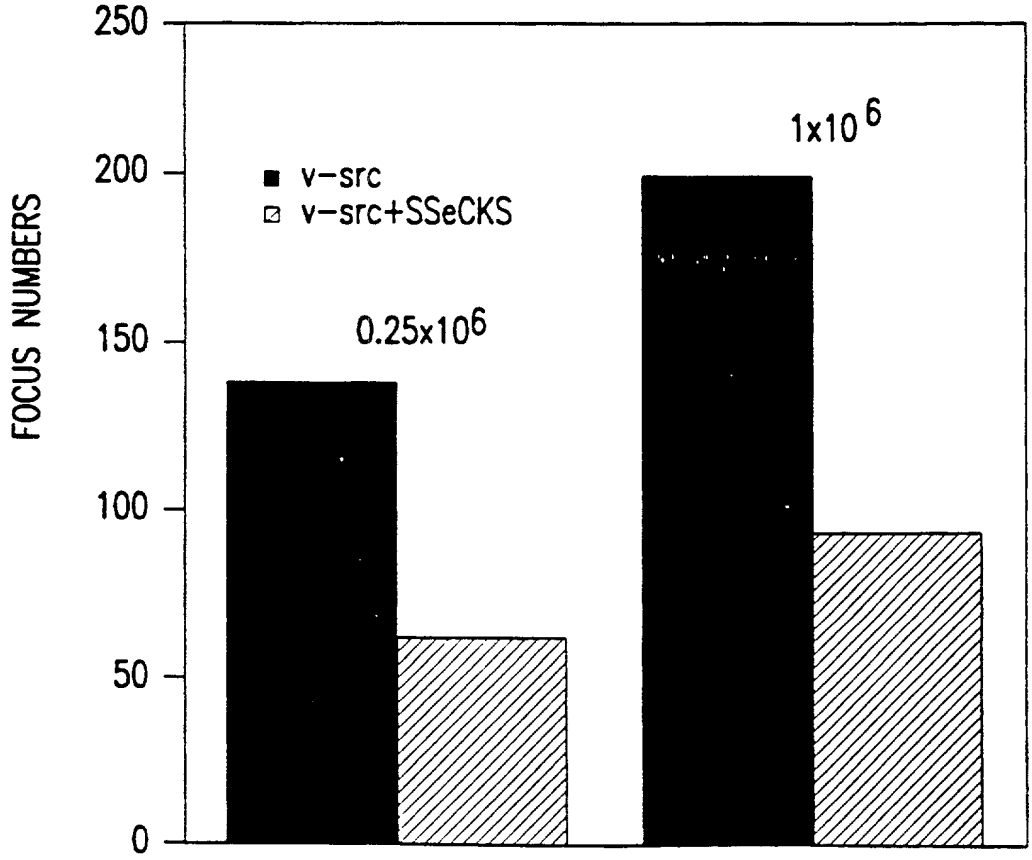


FIG.25B

		Myr.	Pal.
src	MGSSKSKPKD	+	−
yes	MGCIKSKEDK	+	+
SSeCKS	MGAGSSTEQR	+	?
$G_{\alpha t1}$	MGAGASAEEK	+	−
$G_{\alpha i1}$	MGCTLSAEDK	+	+
GAP−43	MLCCMRRTKQ	−	+
MYRIST. CONCENSUS:	MGXXX$^{S}/_{T}$		

FIG.26

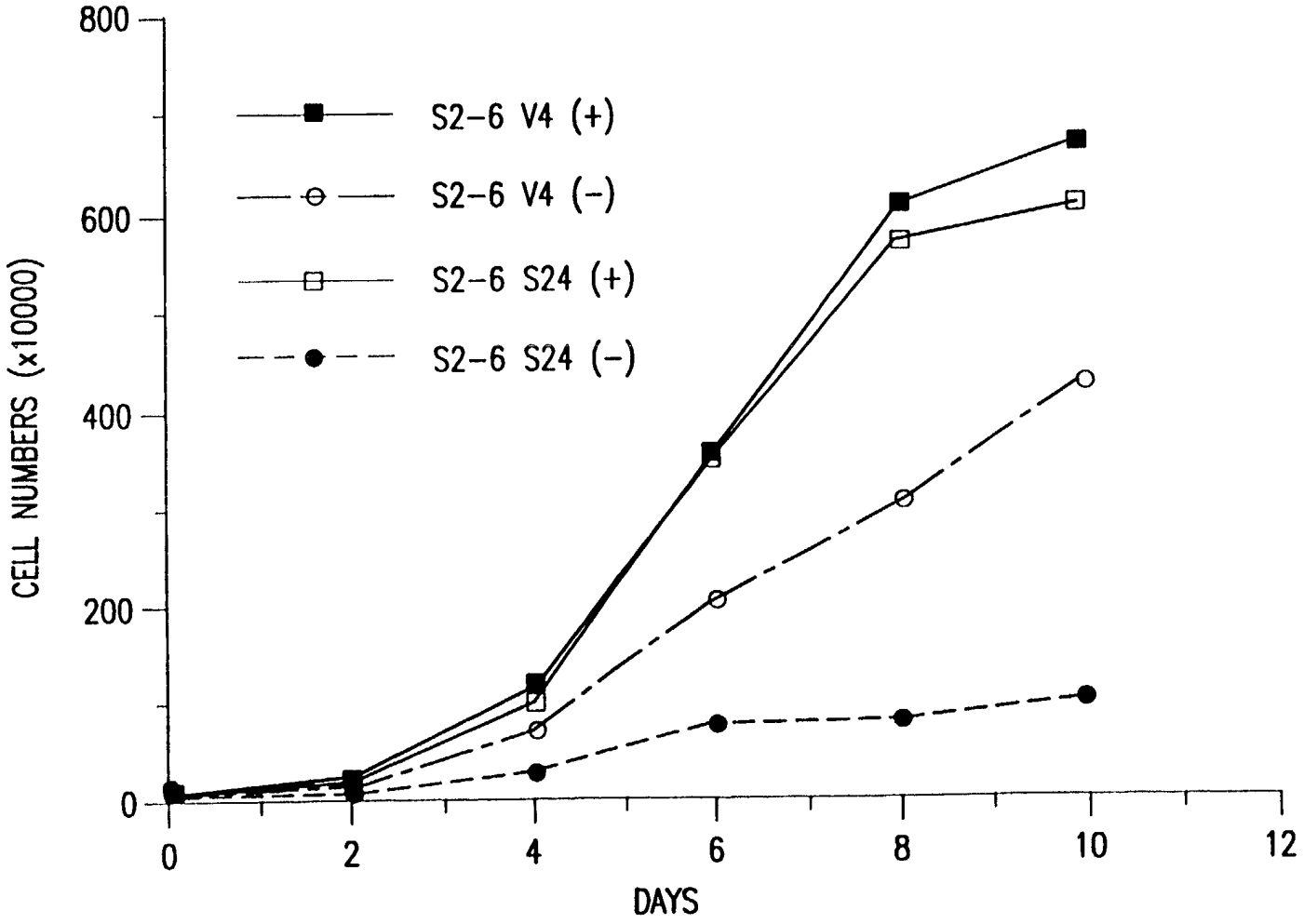

800
600
400
200
0
CELL NUMBERS (x10000)
S2-6 V4 (+)
S2-6 V4 (-)
S2-6 S24 (+)
S2-6 S24 (-)
0
2
4
6
8
10
12
DAYS

FIG.27

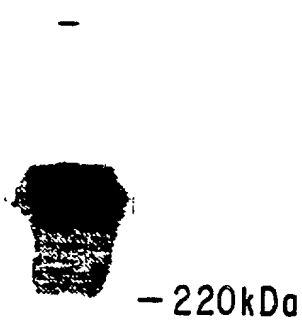


FIG.28

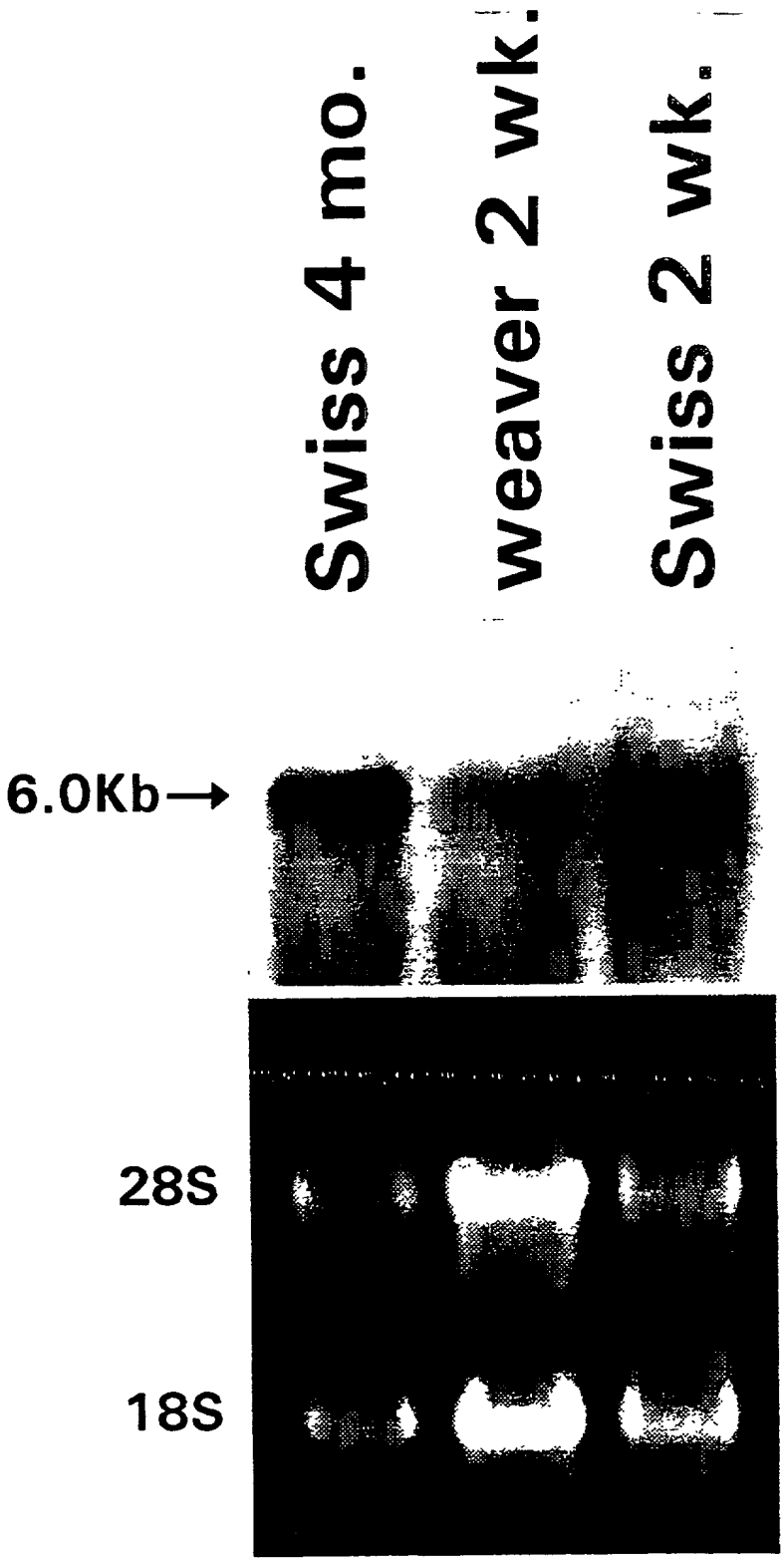


FIG.29

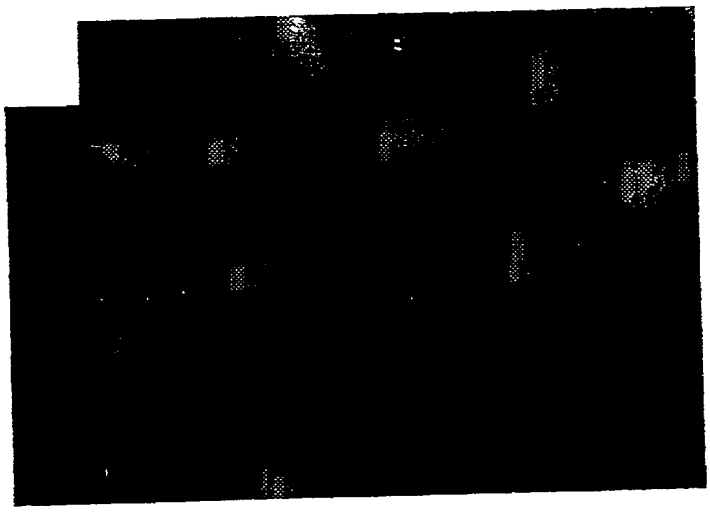


FIG.30A

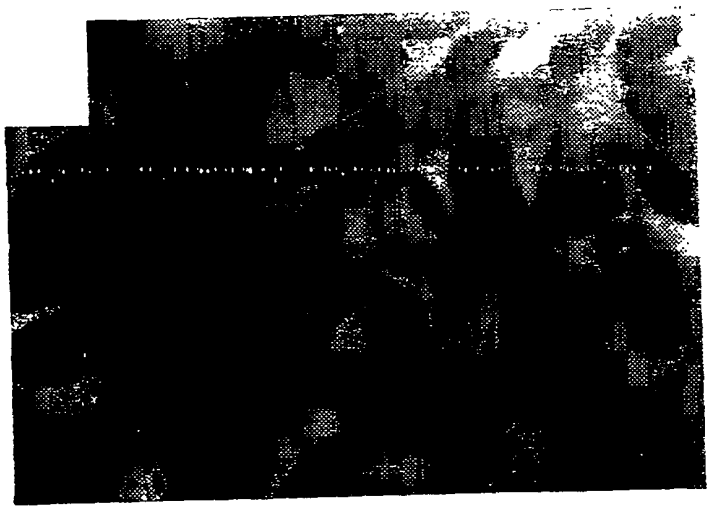


FIG.30B

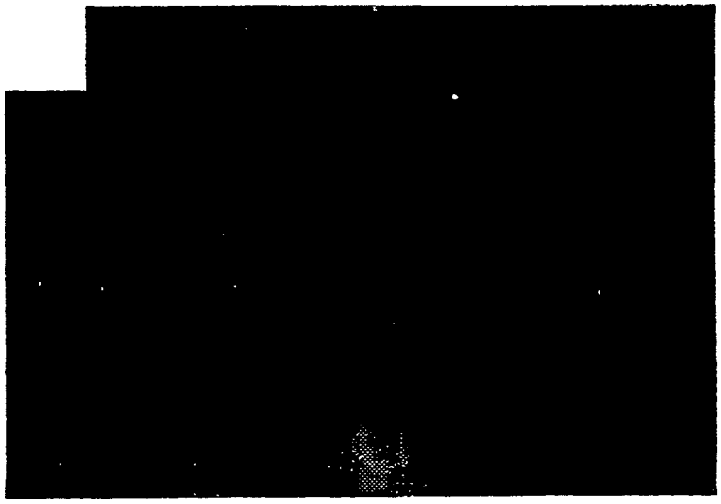


FIG.30C

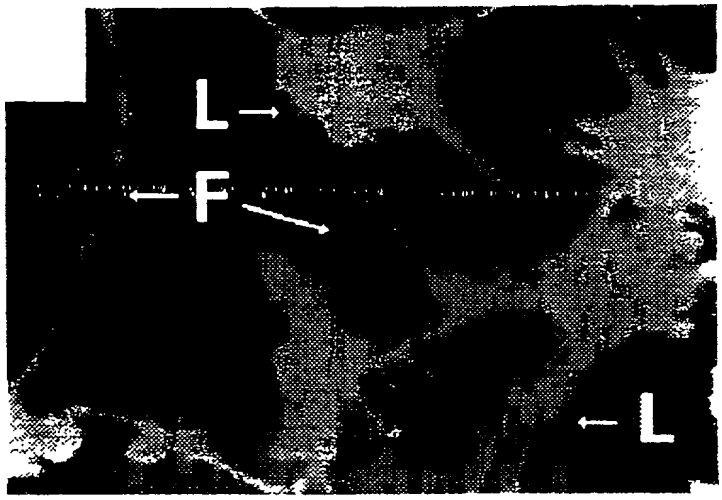


FIG.30D

FIG.31A

FIG.31B

FIG.31C

FIG.31D

FIG.32A

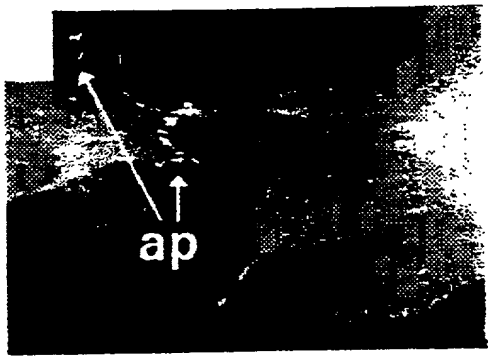


FIG.32B

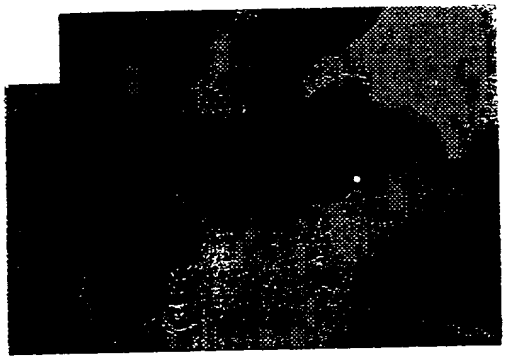


FIG.32C

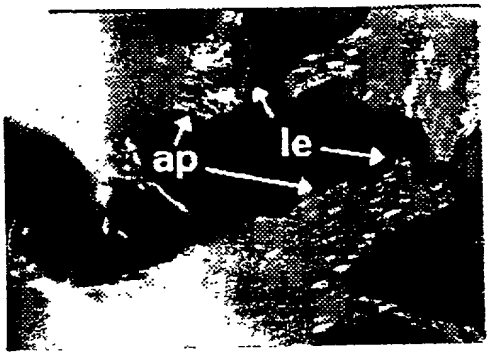


FIG.32D

FIG.32E

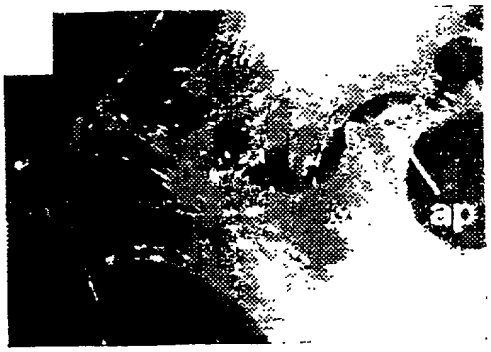


FIG.32F

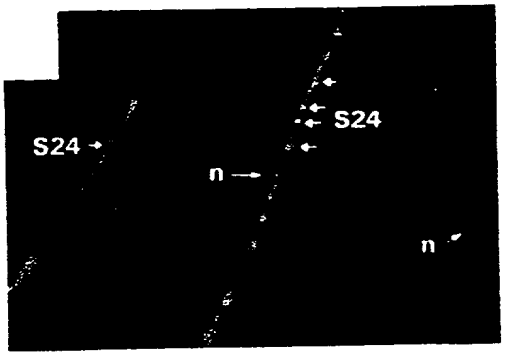


FIG.32G

FIG.32H

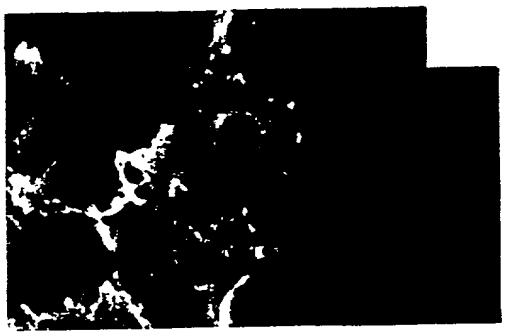


FIG.33A

FIG.33B

FIG.33C

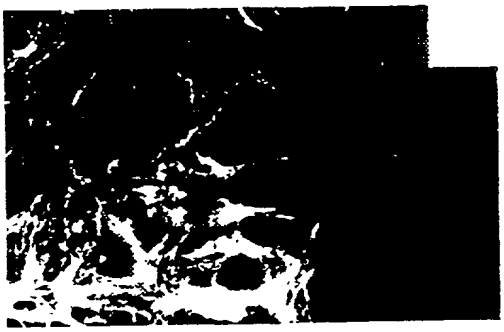


FIG.33D

FIG.33E

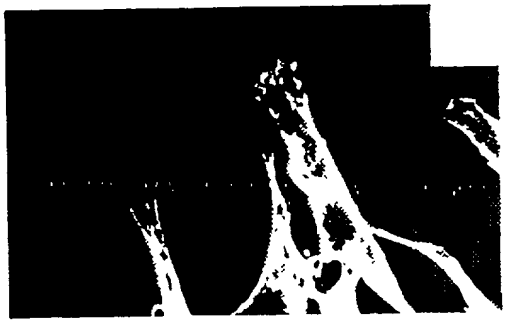


FIG.33F

FIG.33G

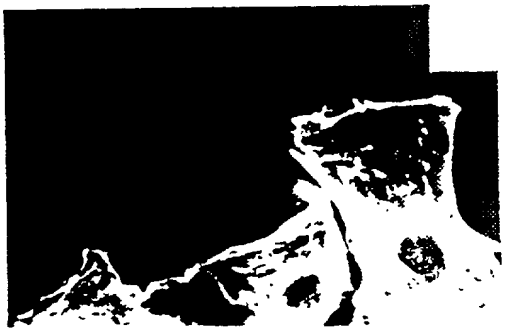


FIG.33H

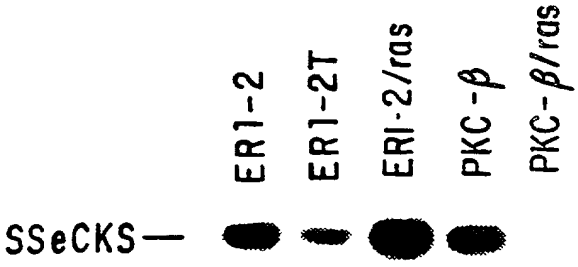


FIG.34

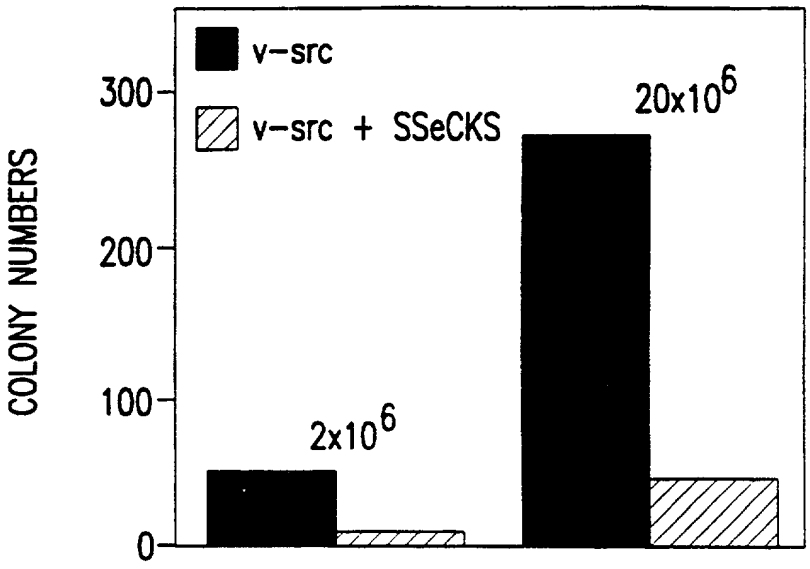


FIG.35A

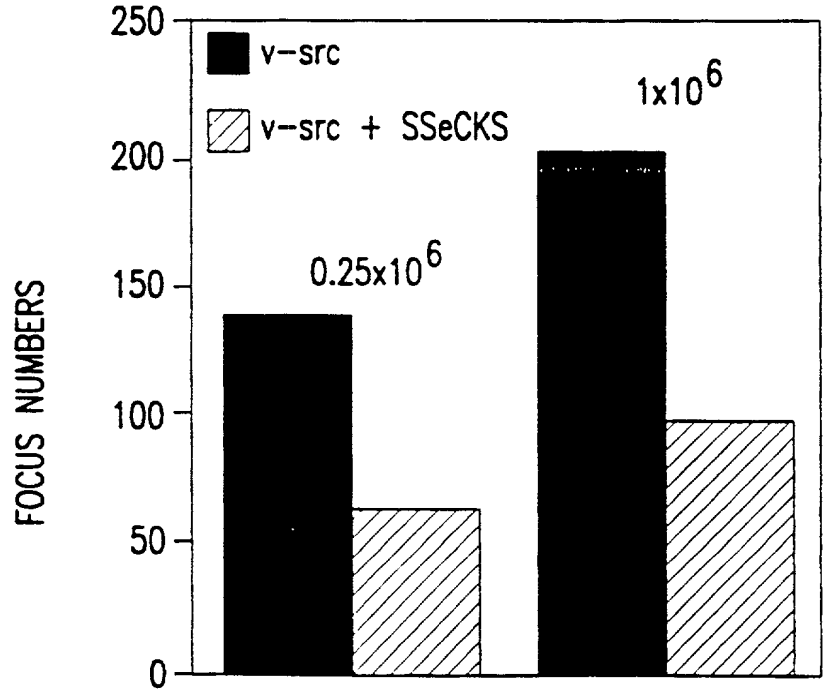


FIG.35B

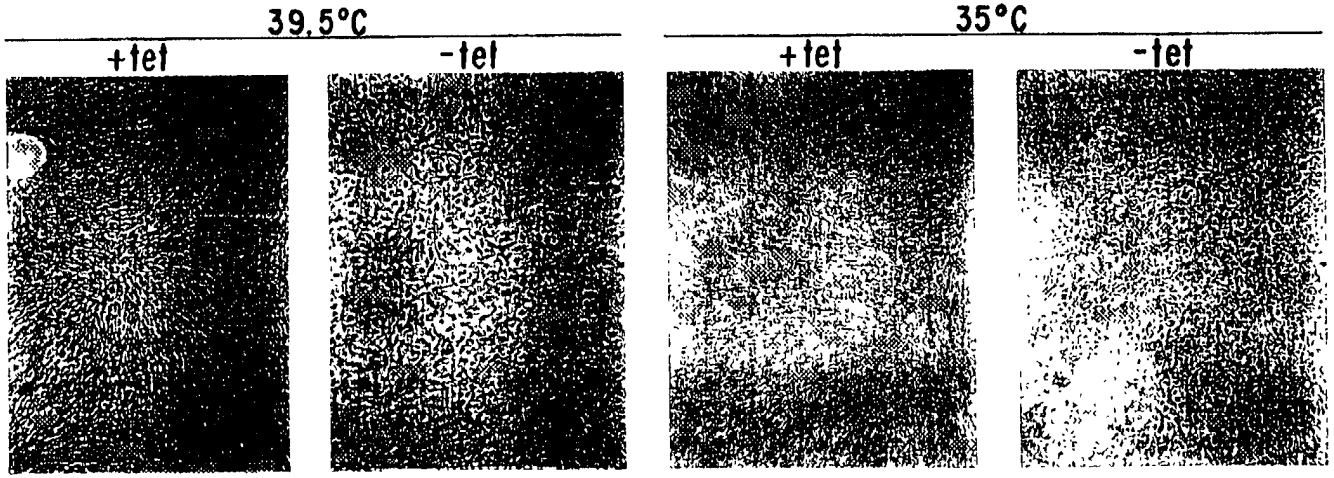


FIG.36A-1 FIG.36A-2 FIG.36A-3 FIG.36A-4

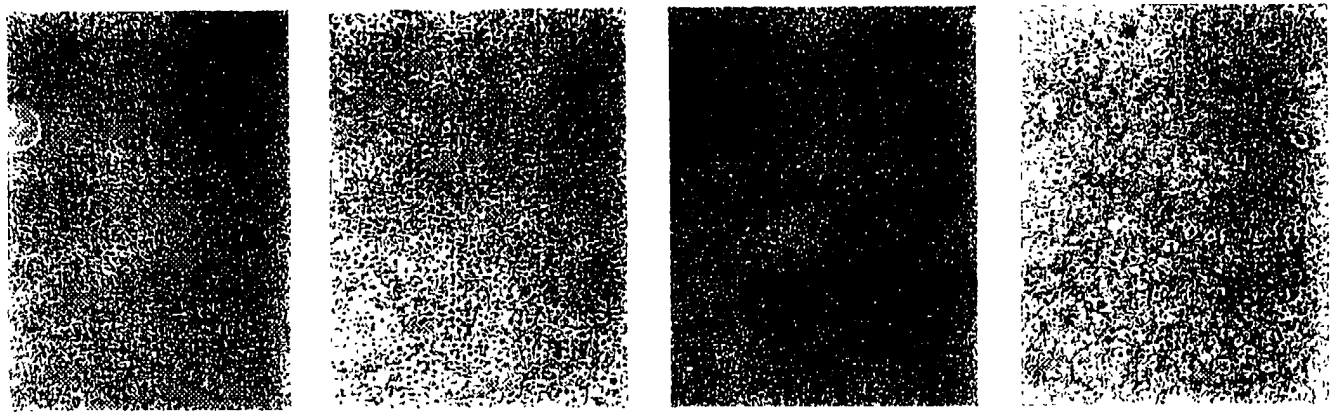


FIG.36A-5 FIG.36A-6 FIG.36A-7 FIG.36A-8

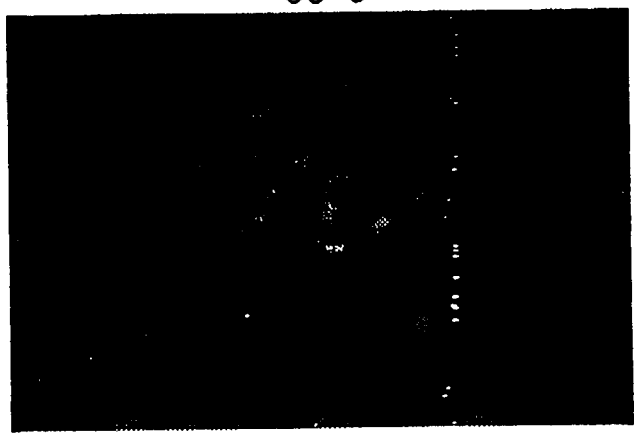


FIG.36B-1

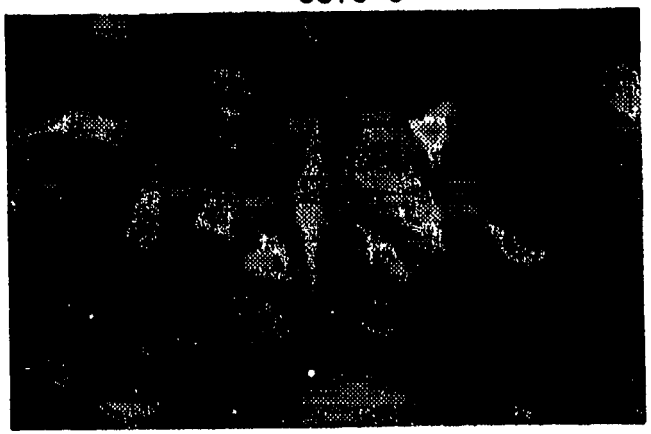


FIG.36B-2

FIG.36B-3

FIG.36B-4

FIG.37A-1

FIG.37A-2

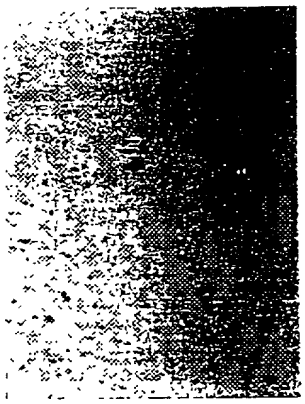


FIG.37A-3

FIG.37A-4

SOFT AGAR COLONY FORMATION						
	ts src1	ts src2	ts src3	ts src4	pLJ2	pLJ3
+ tet	2160	1640	2800	1080	0	0
− tet	60	60	110	35	0	0

FIG.37B

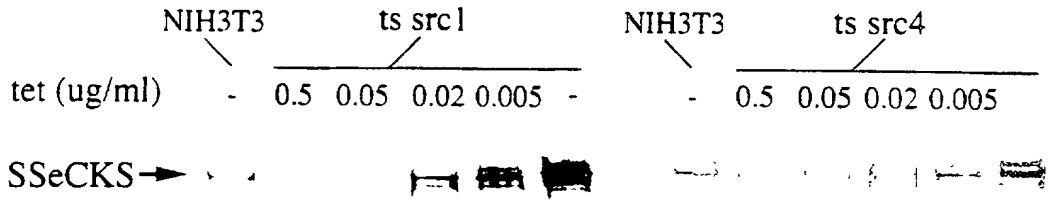


FIG.38A

FIG.38C-1

FIG.38C-2

SOFT AGAR COLONY FORMATION							
	35°C					39°C	
tet(ug/ml)	0.5	0.05	0.02	0.005	0	0.5	0
ts src1	2852	2464	174	51	22	0	0
ts src4	1463	743	67	11	0	0	0

FIG.38B

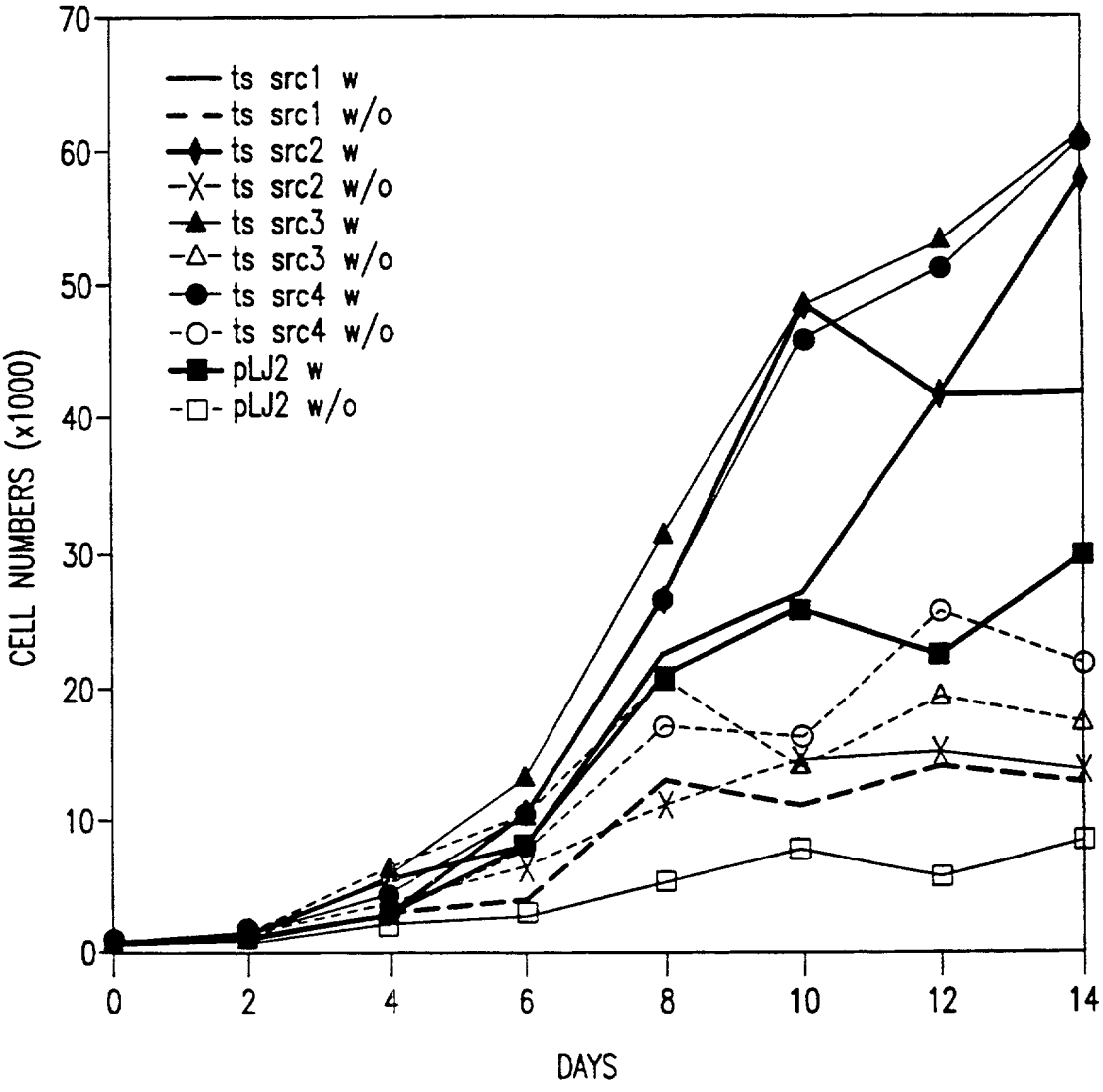

70
60
50
40
30
20
10
0
CELL NUMBERS (x1000)
ts src1 w
ts src1 w/o
ts src2 w
ts src2 w/o
ts src3 w
ts src3 w/o
ts src4 w
ts src4 w/o
pLJ2 w
pLJ2 w/o
0
2
4
6
8
10
12
14
DAYS

FIG.39A

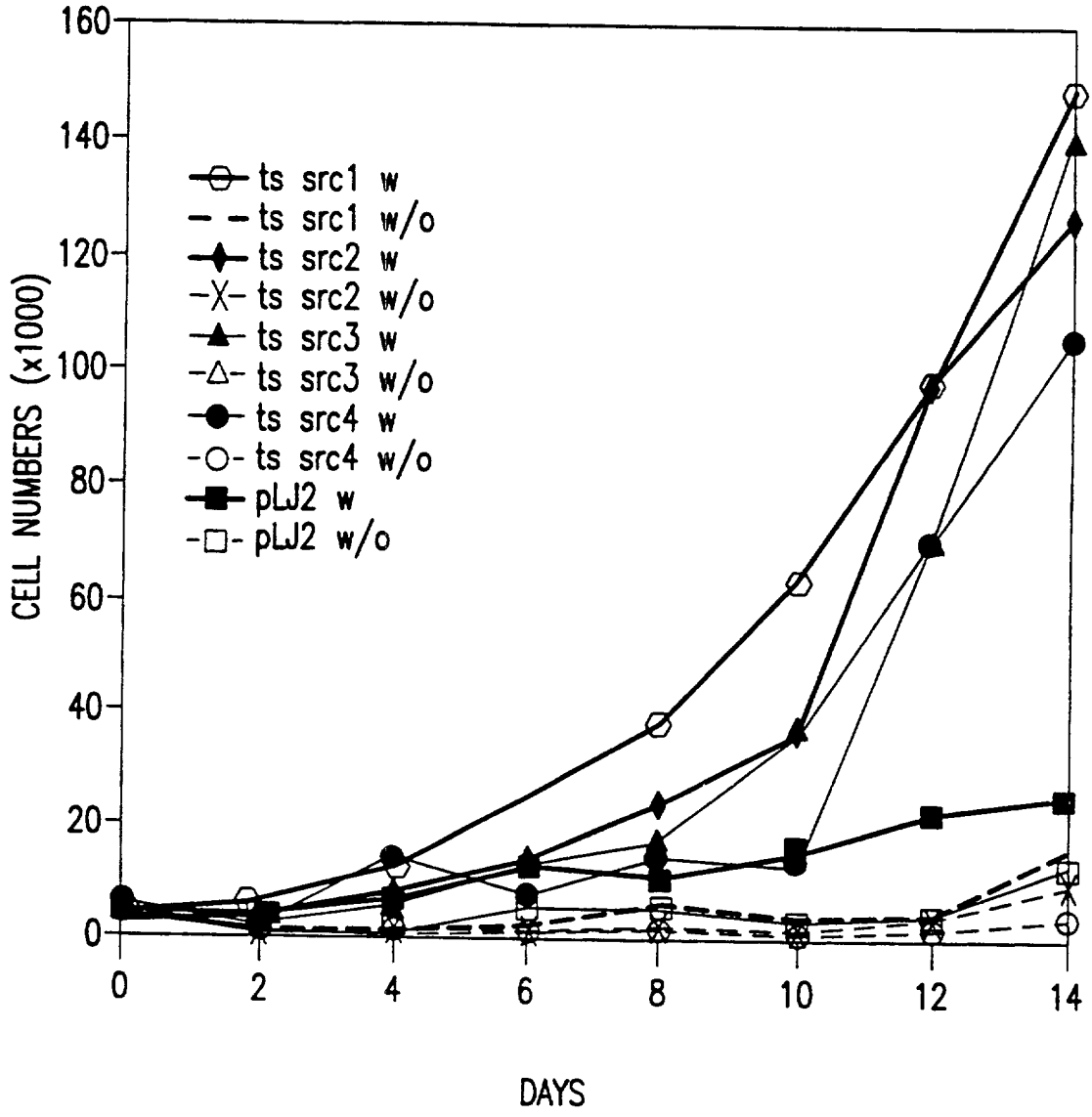

160
140
120
100
80
60
40
20
0
CELL NUMBERS (x1000)
ts src1 w
ts src1 w/o
ts src2 w
ts src2 w/o
ts src3 w
ts src3 w/o
ts src4 w
ts src4 w/o
pLJ2 w
pLJ2 w/o
0
2
4
6
8
10
12
14
DAYS

FIG.39B

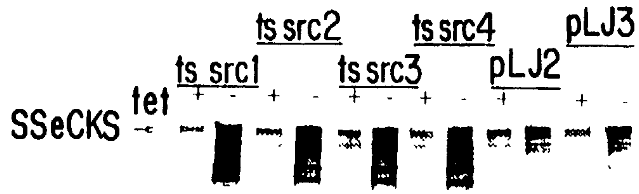


FIG.40A

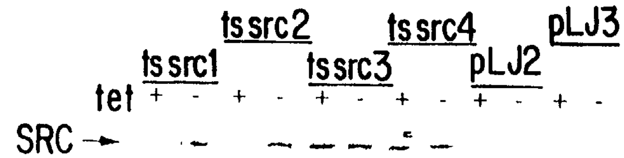


FIG.40B

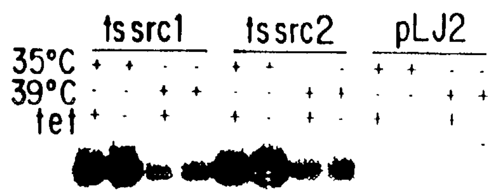


FIG.40C-1

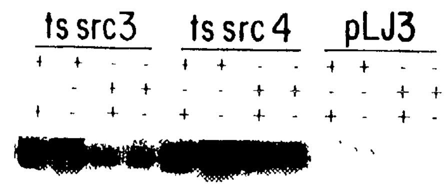


FIG.40C-2

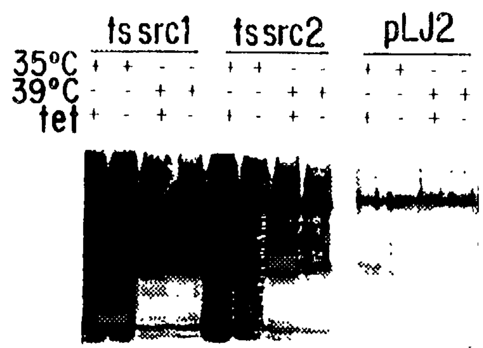


FIG.40D-1

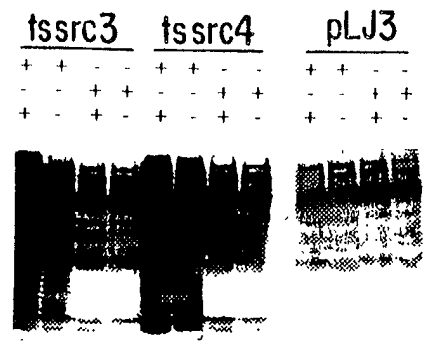


FIG.40D-2

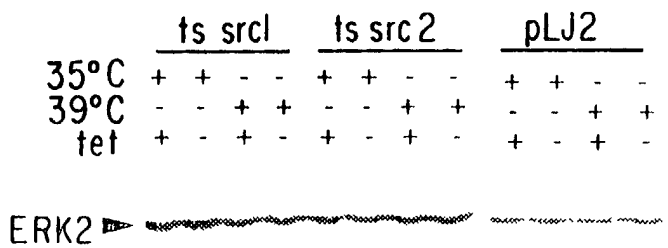


FIG.41A-1

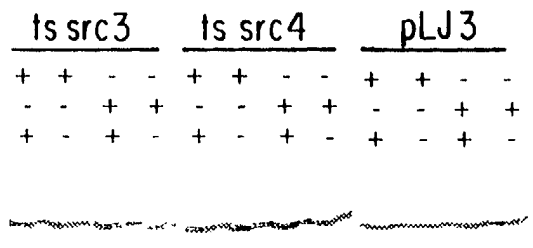


FIG.41A-2

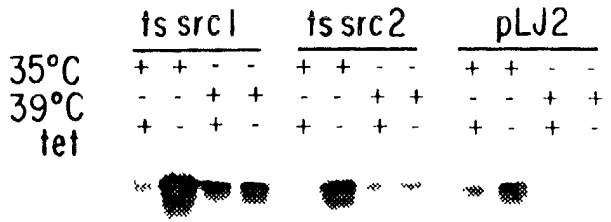


FIG.41B-1

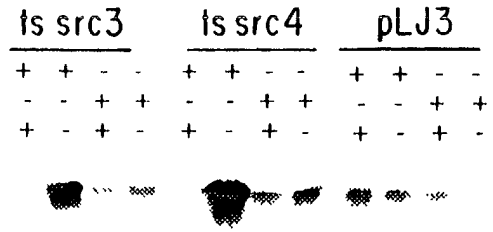


FIG.41B-2

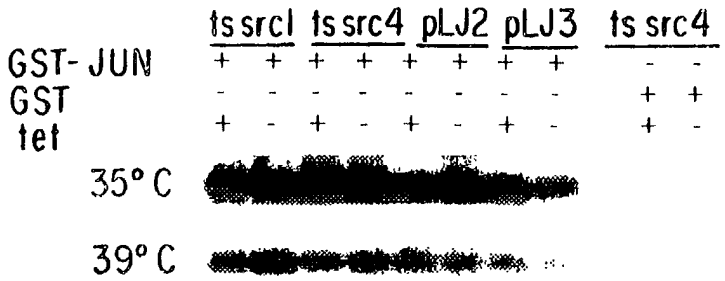


FIG.41C

(as of 89)

SSeCKS

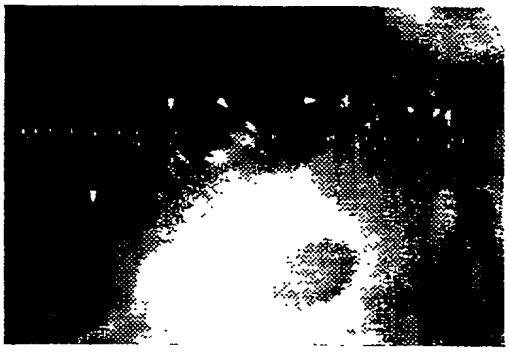
FIG.42A-1

Vinculin

35°C
+tet

FIG.42A-2

FIG.42A-3



35°C
-tet

FIG.42A-4

SSeCKS

FIG.42A-5

Vinculin

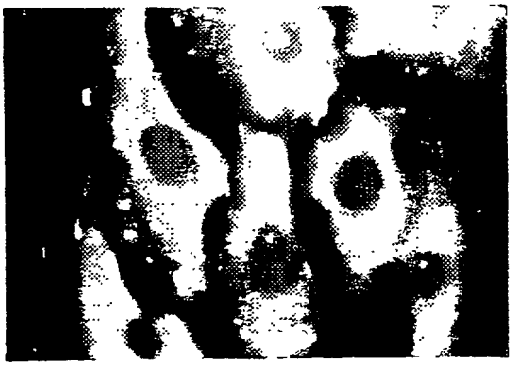


FIG.42A-6

FIG.42A-7

FIG.42A-8

SSeCKS

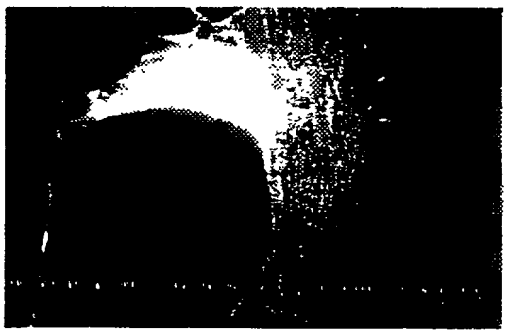
FIG.42B-1

Phalloidin

35°C
+tet

FIG.42B-2

FIG.42B-3



35°C
−tet

FIG.42B-4

SSeCKS

FIG.42B-5

Phalloidin

FIG.42B-6

FIG.42B-7

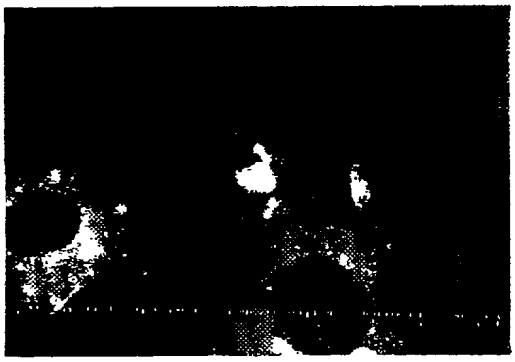


FIG.42B-8

Figure 43

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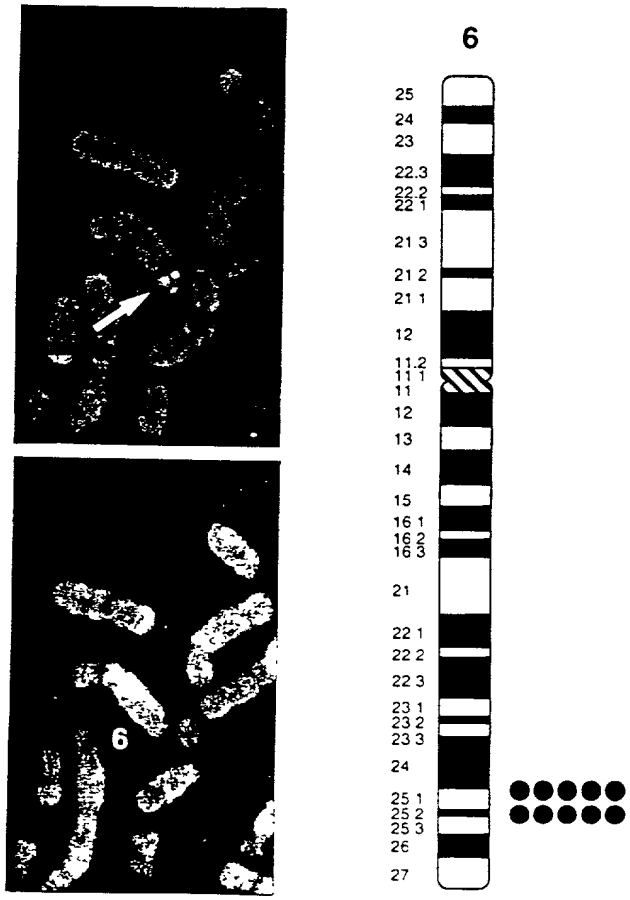

Figure 44

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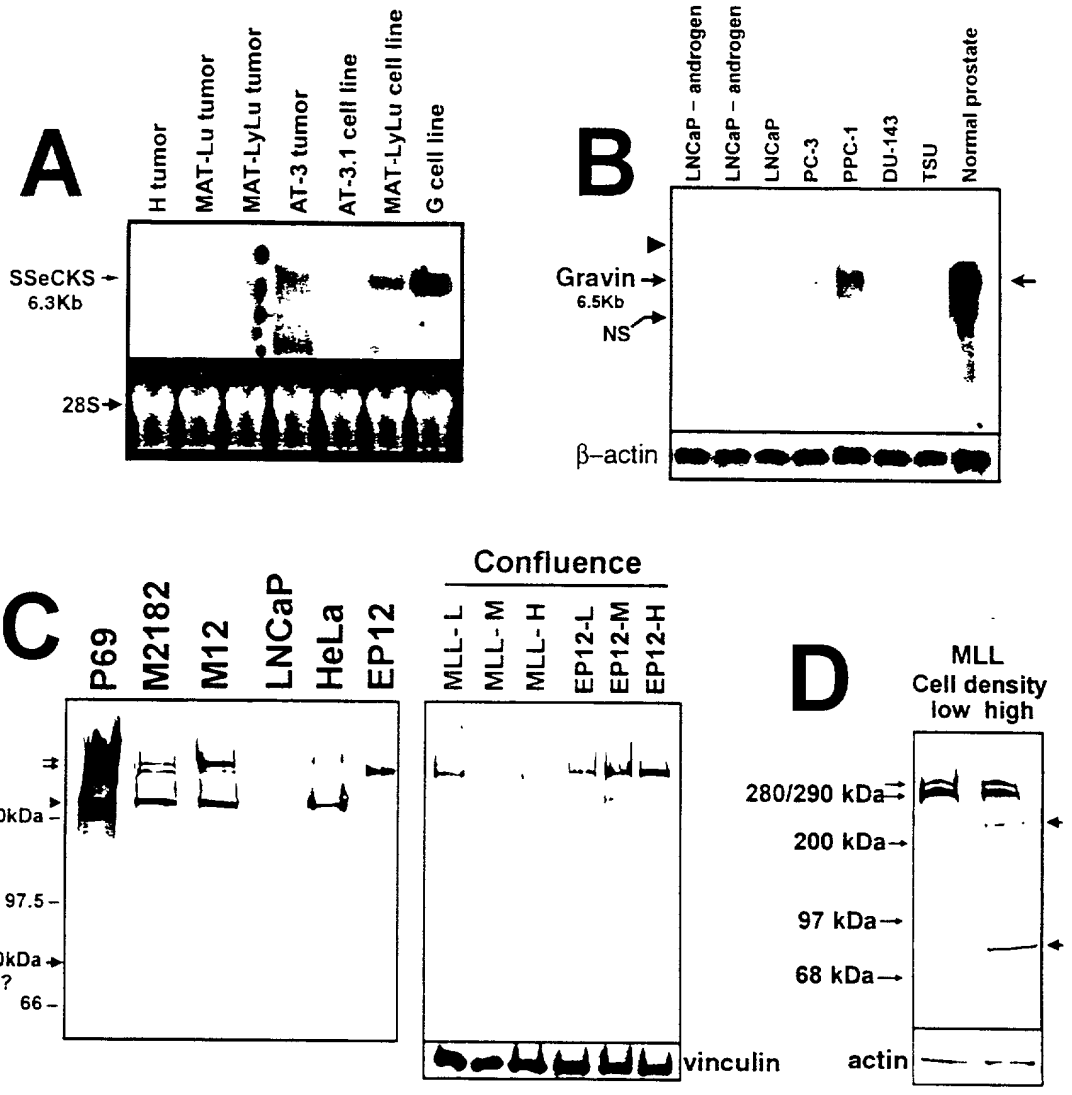

Figure 45

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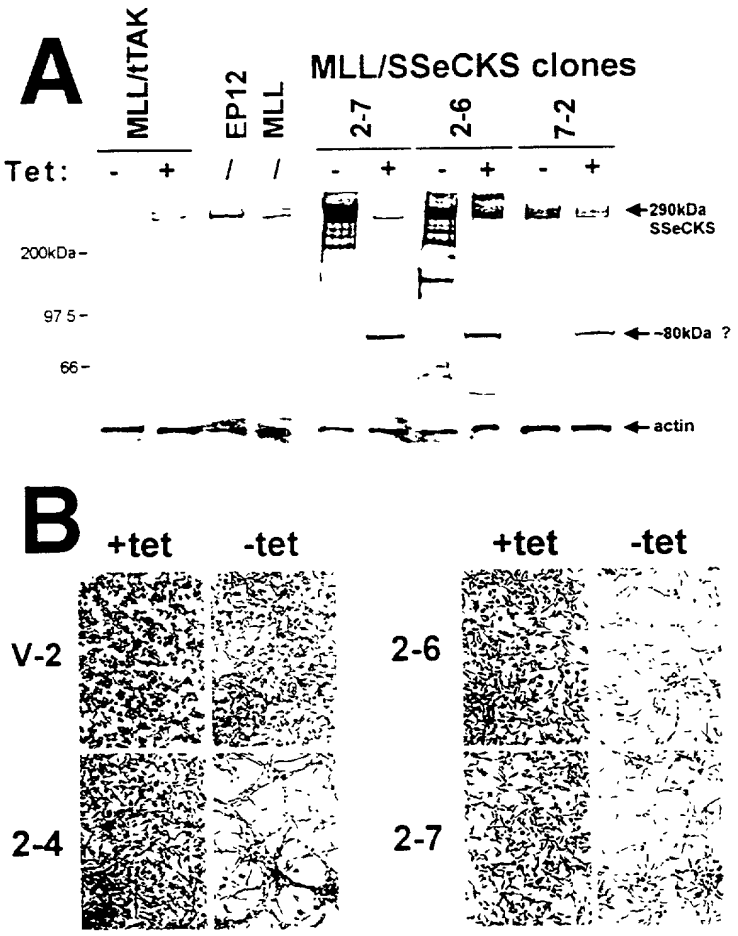

Figure 46

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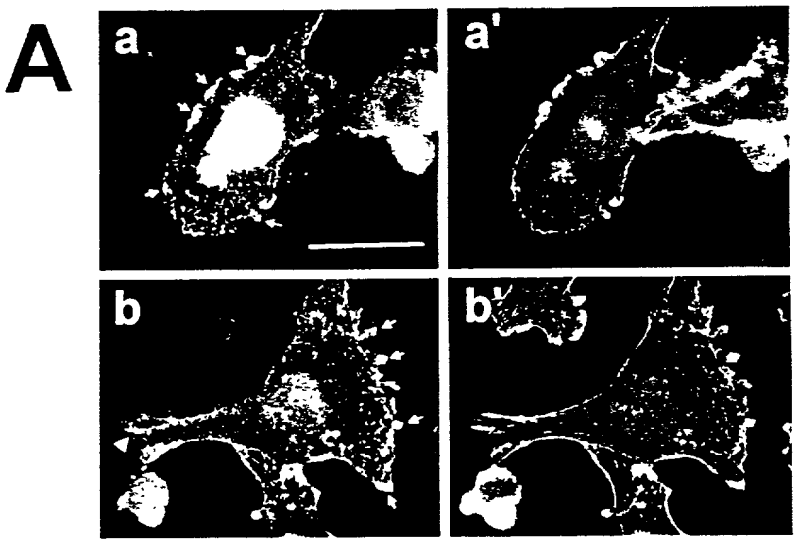
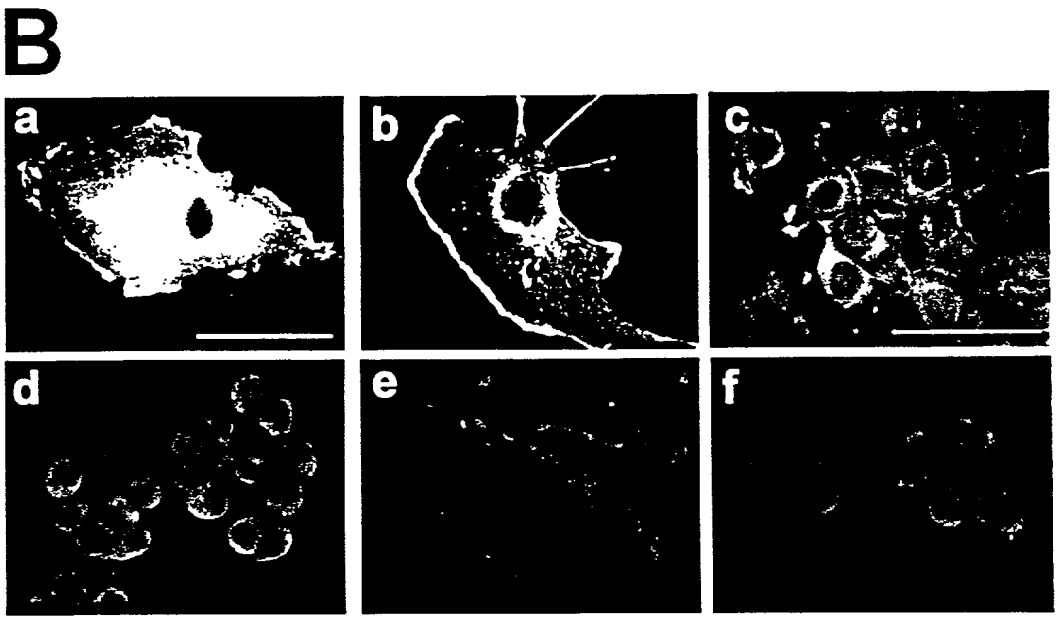
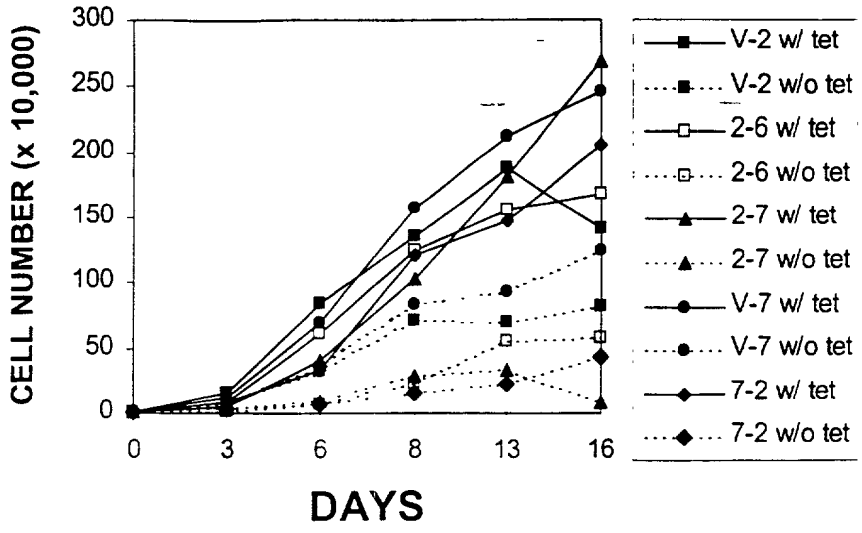
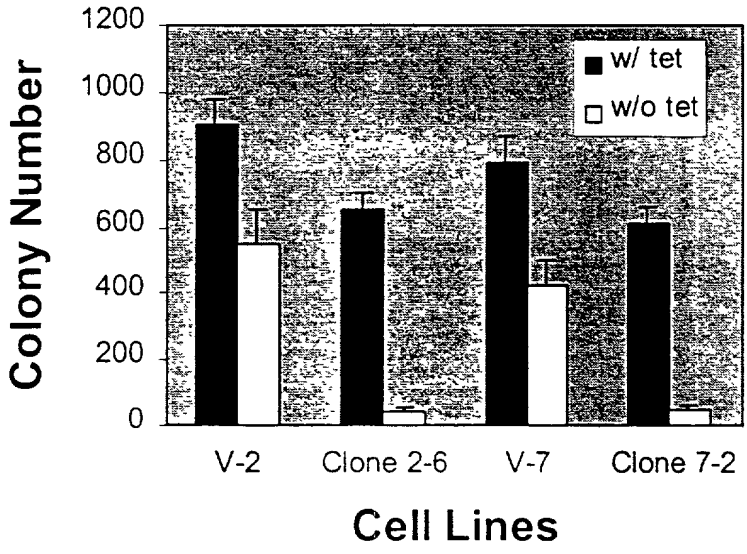




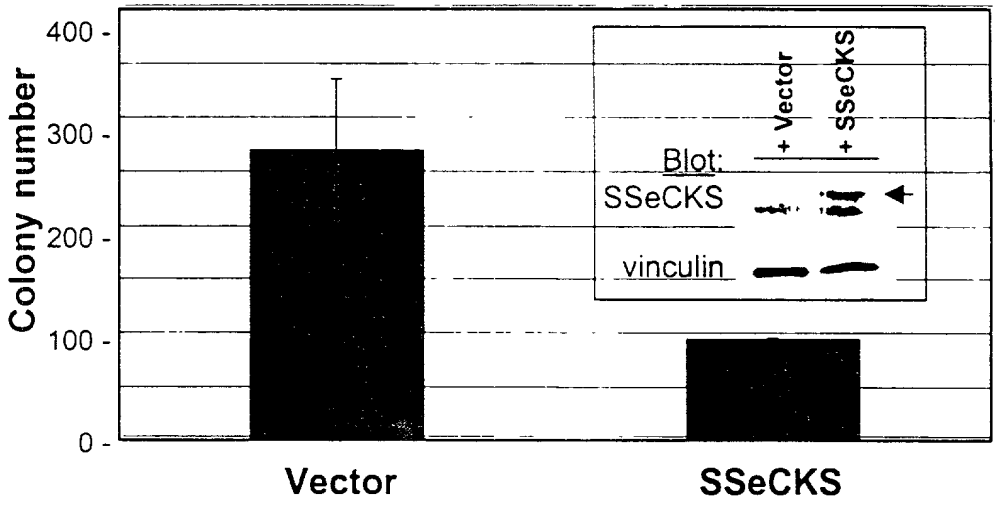
A

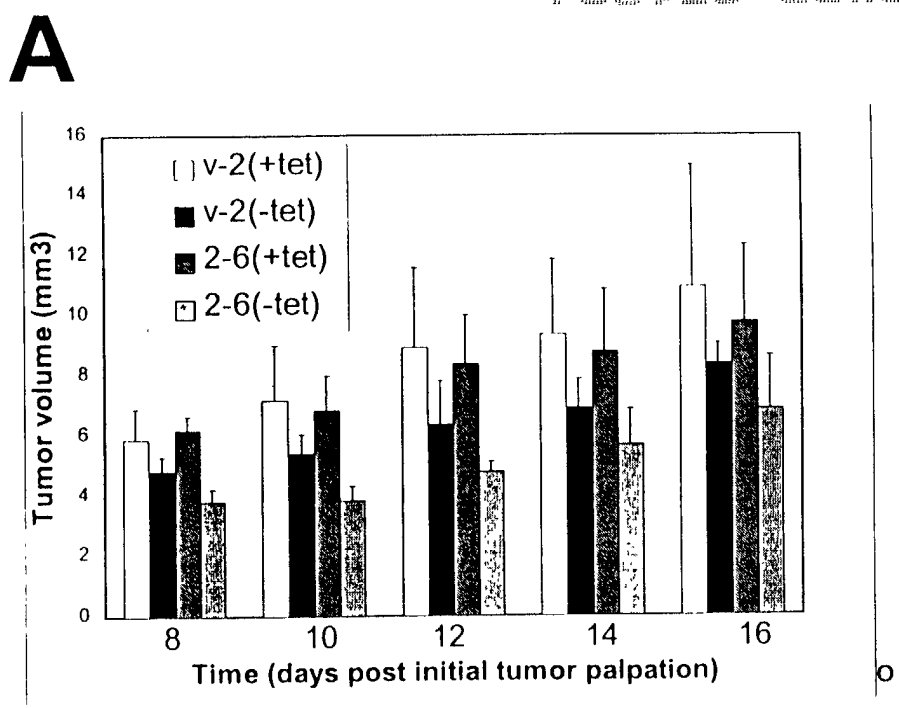

CELL NUMBER (x 10,000)
300
250
200
150
100
50
0
0
3
6
8
13
16
DAYS
V-2 w/ tet
V-2 w/o tet
2-6 w/ tet
2-6 w/o tet
2-7 w/ tet
2-7 w/o tet
V-7 w/ tet
V-7 w/o tet
7-2 w/ tet
7-2 w/o tet

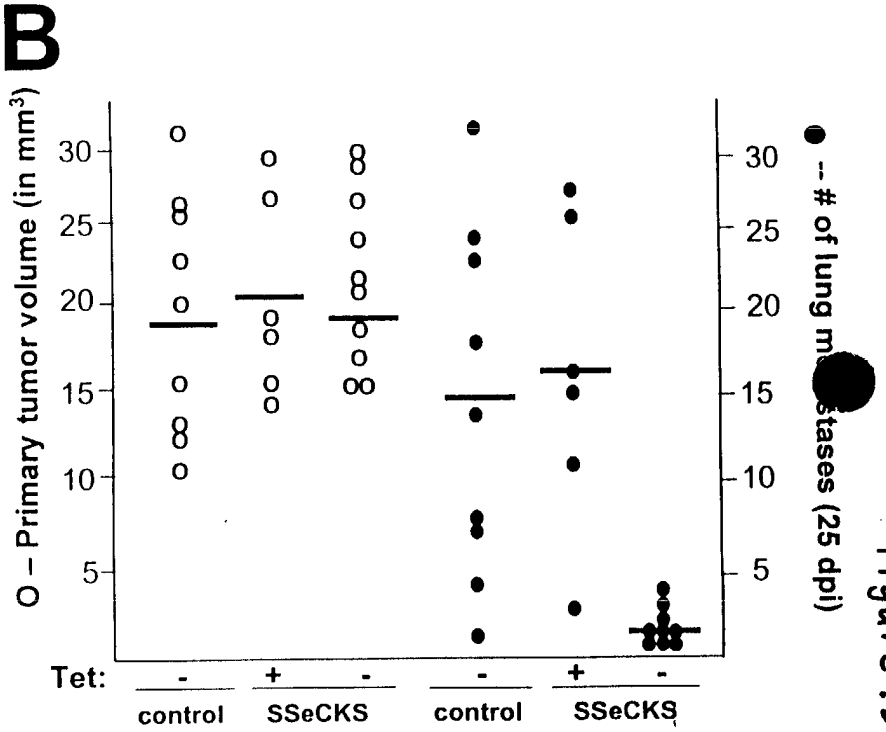
B

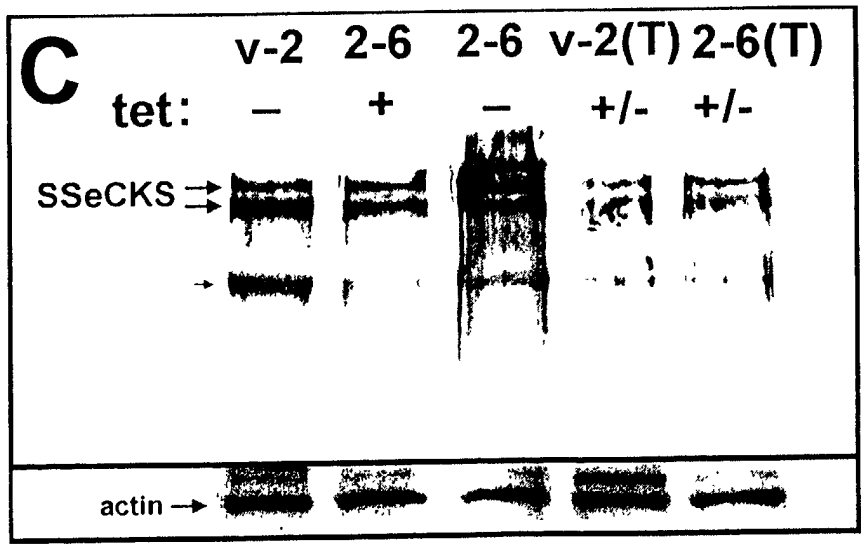

Colony Number
1200
1000
800
600
400
200
0
w/ tet
w/o tet
V-2
Clone 2-6
V-7
Clone 7-2
Cell Lines

C


Colony number
400
300
200
100
0
+ Vector
+ SSeCKS
Blot:
SSeCKS
vinculin
Vector
SSeCKS







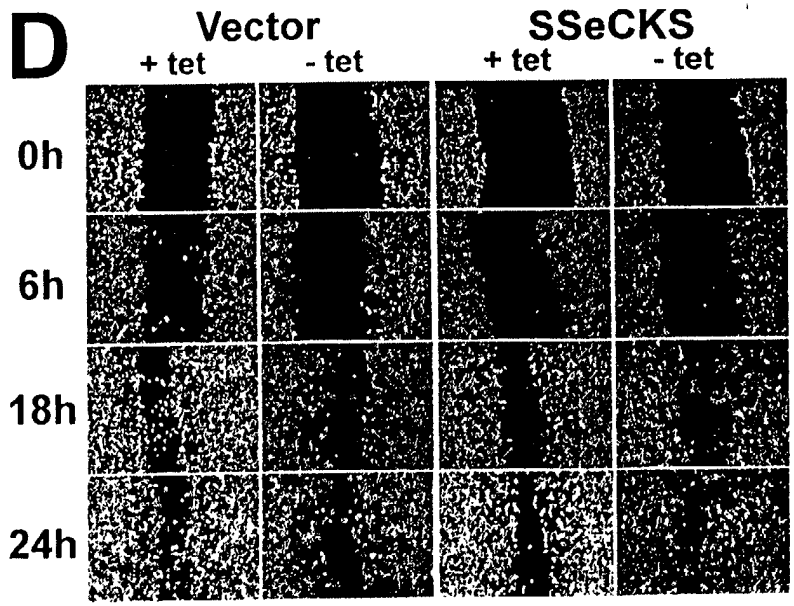


Figure 48 (78 of 90)

Figure 49

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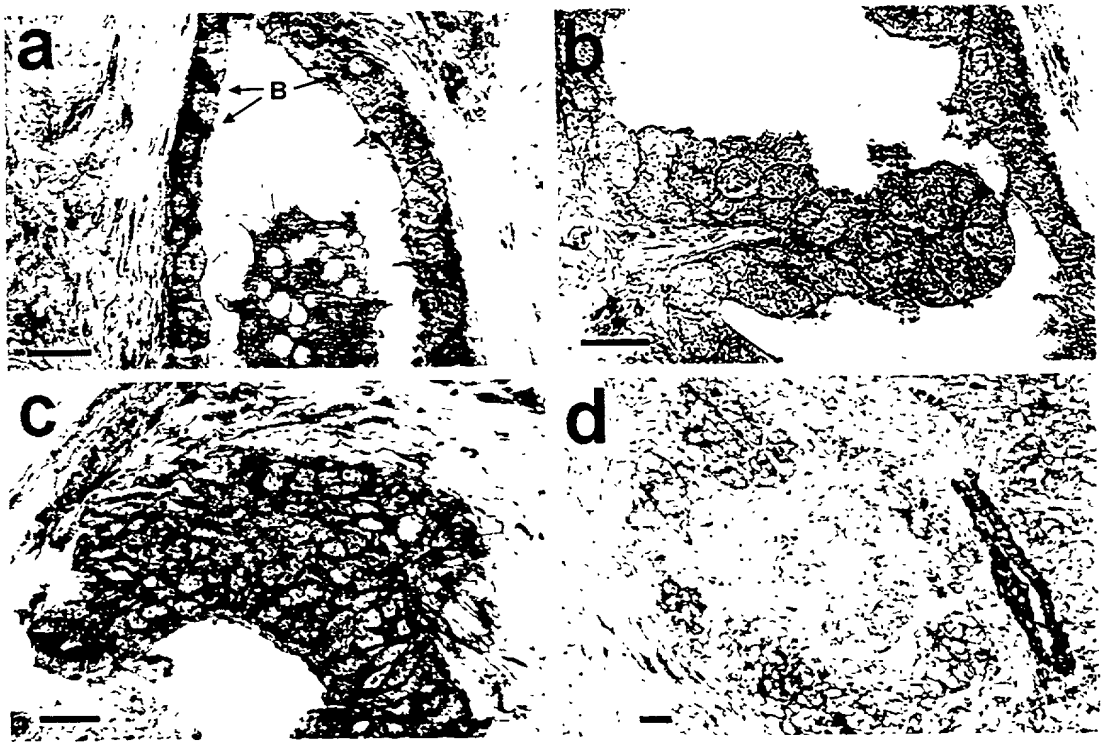

Figure 50

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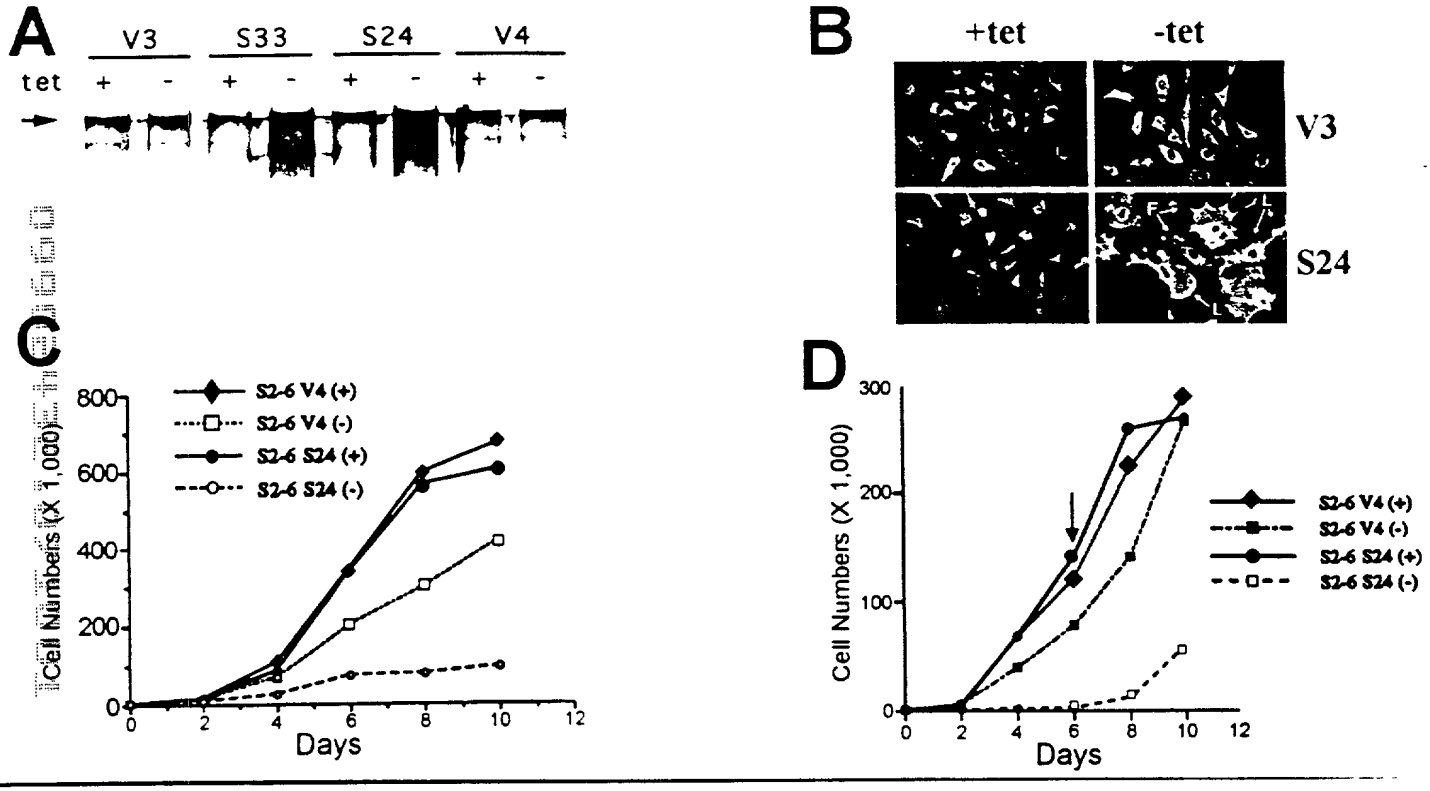

Figure 51

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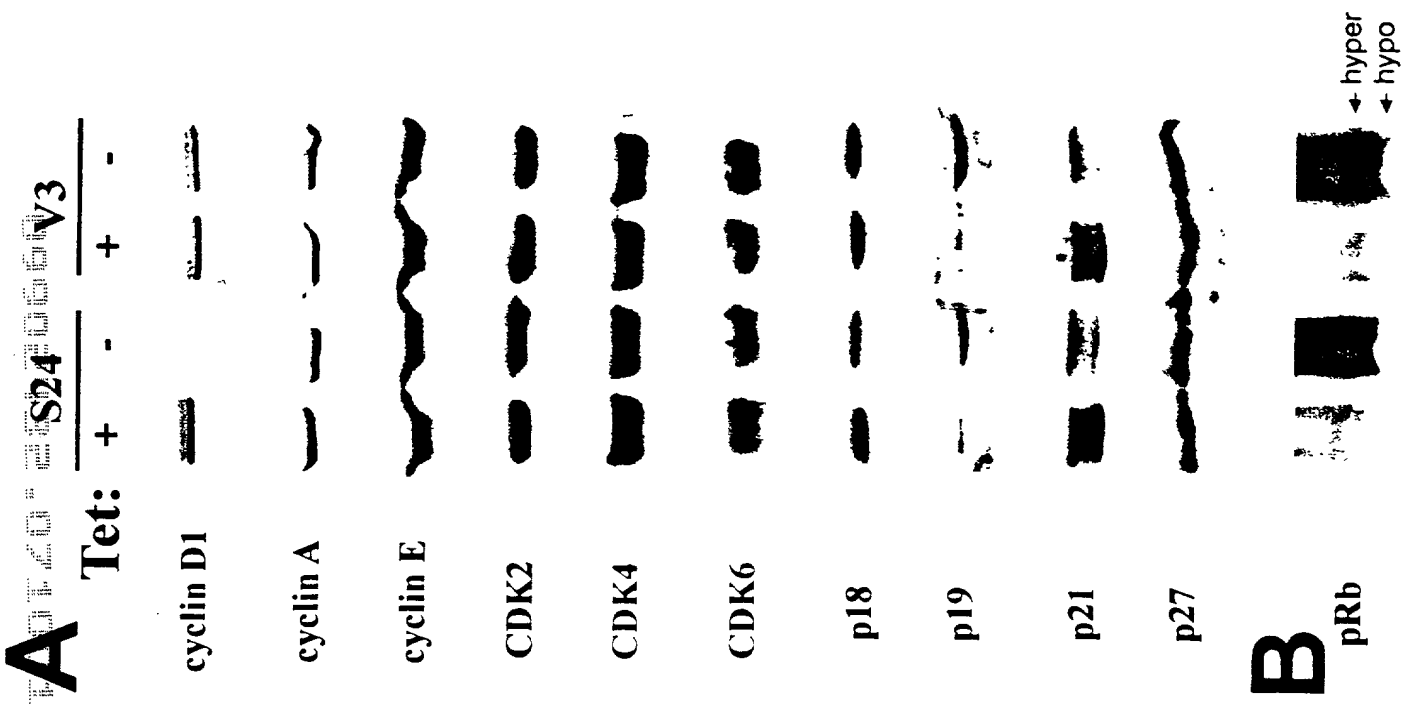

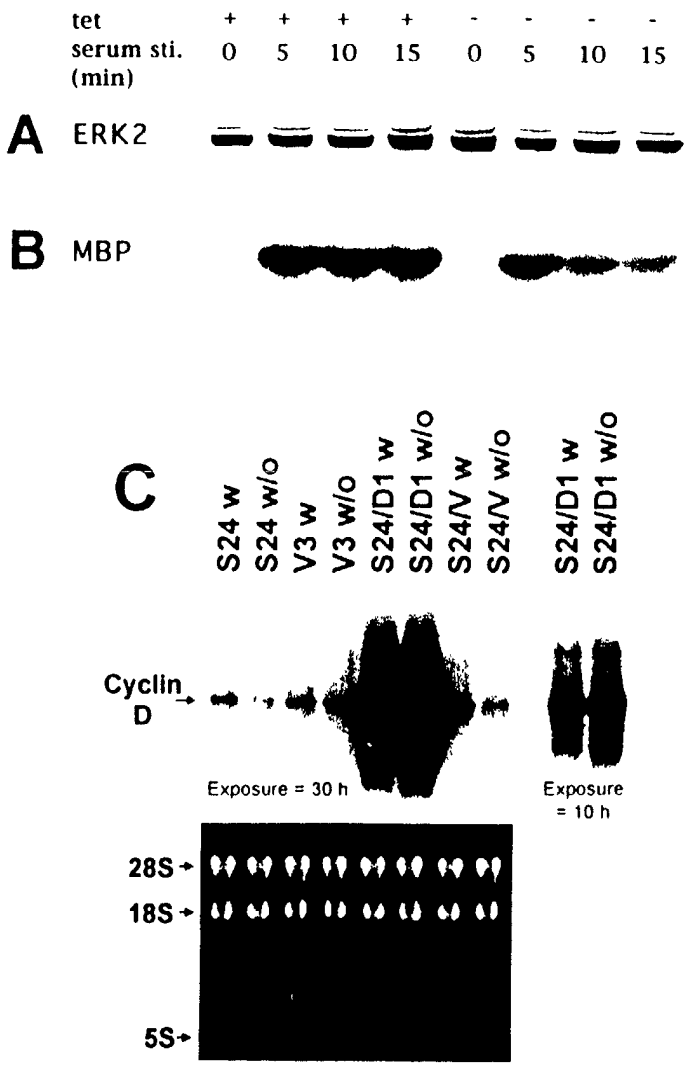

Figure 52

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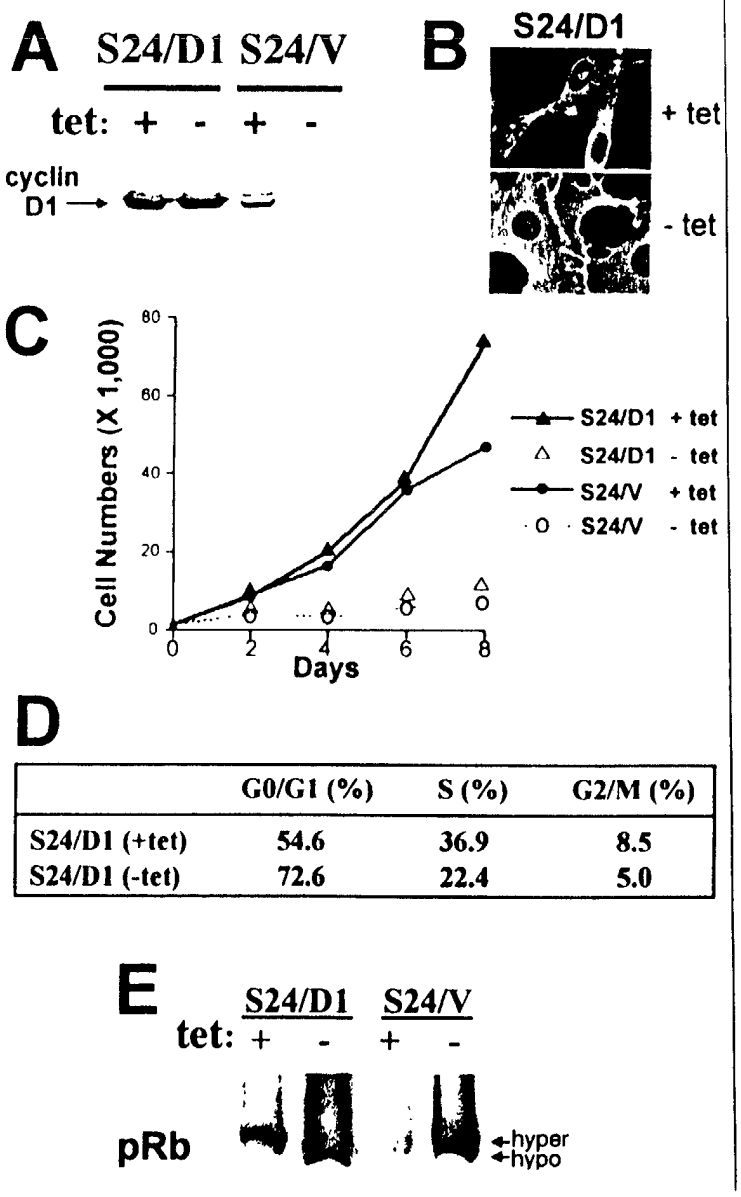

	G0/G1 (%)	S (%)	G2/M (%)
S24/D1 (+tet)	54.6	36.9	8.5
S24/D1 (-tet)	72.6	22.4	5.0

Figure 53

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Figure 54


```
SSeCKS      468SPEEKTLPKHPEGIVSEVEM                LSSQERIK496
               ||  ||: |||||::|    |                 ||| ||::
Newt pRb    780SP.LKSPYKHPEGLLSPTKM -(27 a.a.)- LSSSERLR834
```

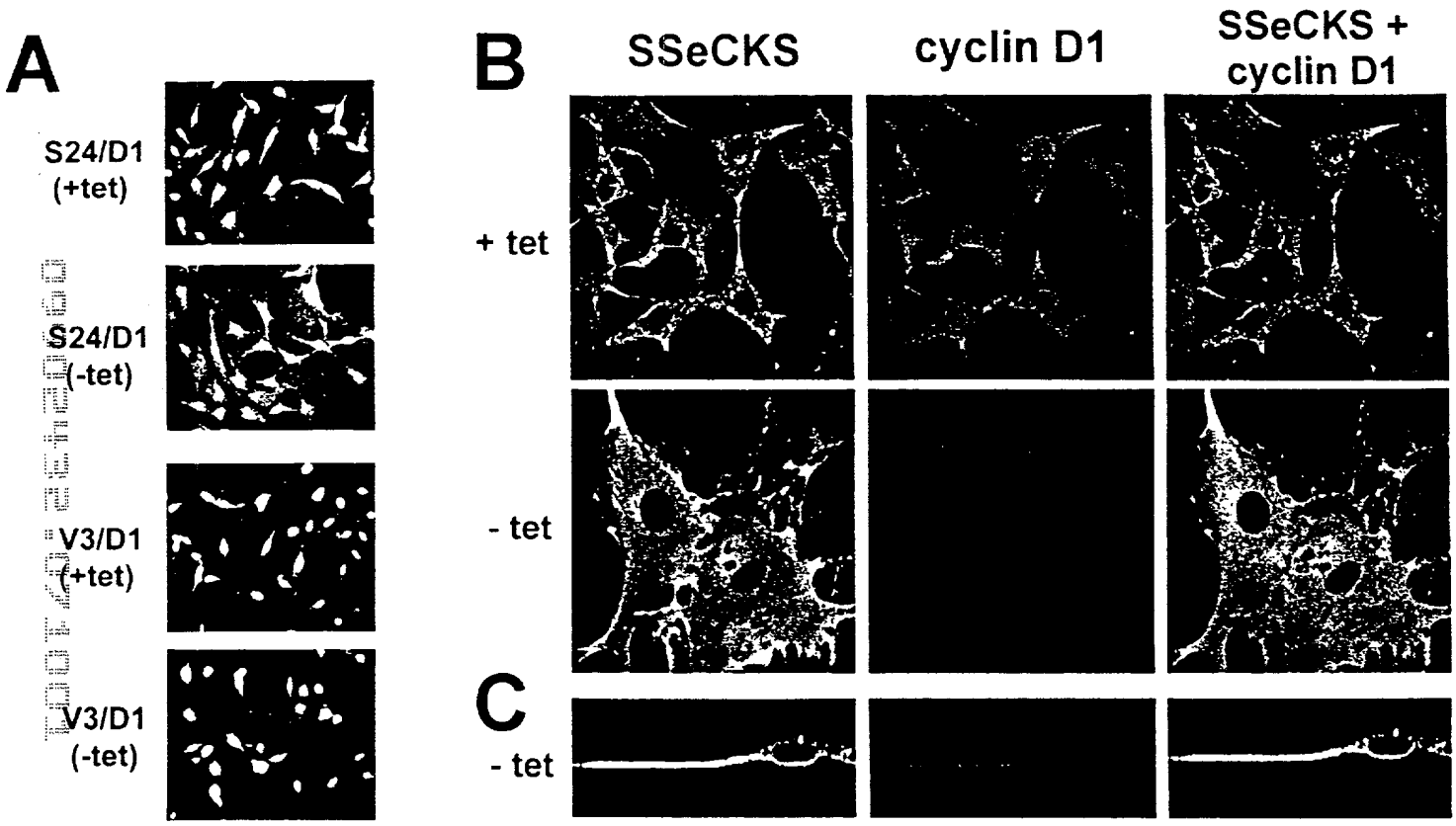
A
S24/D1 (+tet)
S24/D1 (-tet)
V3/D1 (+tet)
V3/D1 (-tet)
B
SSeCKS
cyclin D1
SSeCKS + cyclin D1
+ tet
- tet
C
- tet

Figure 56

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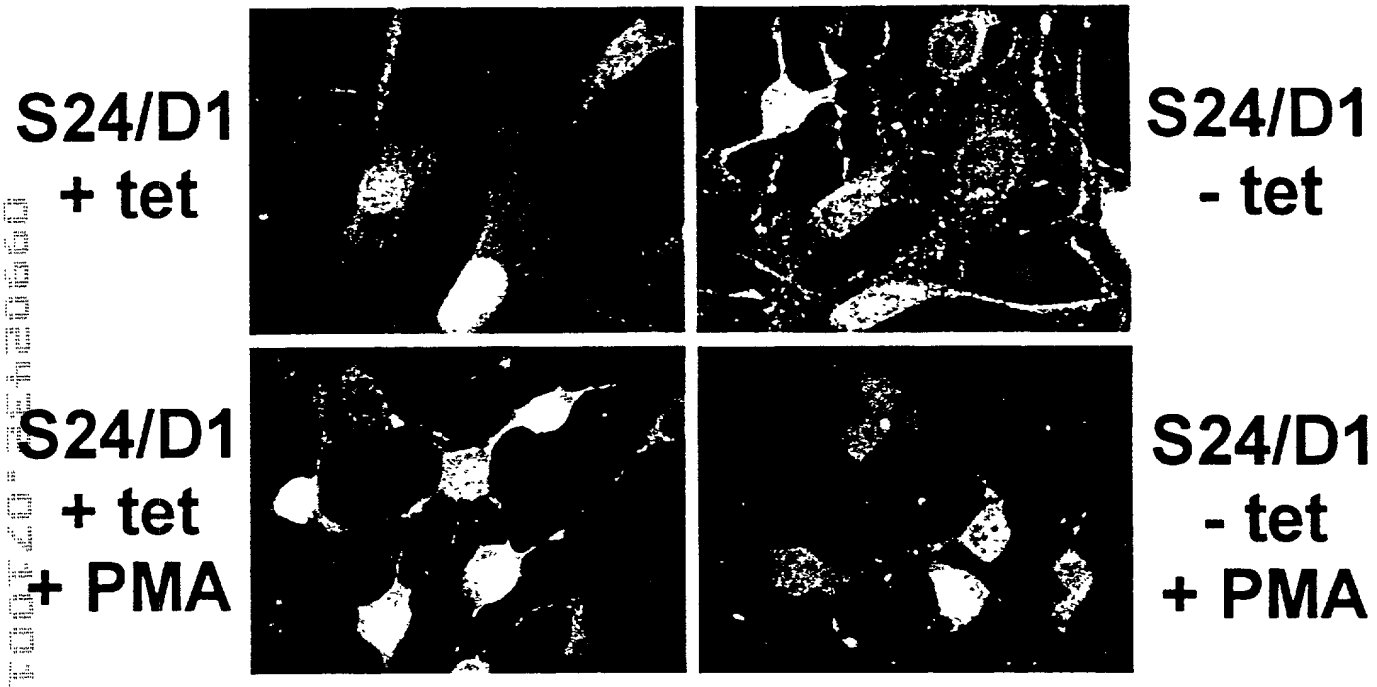

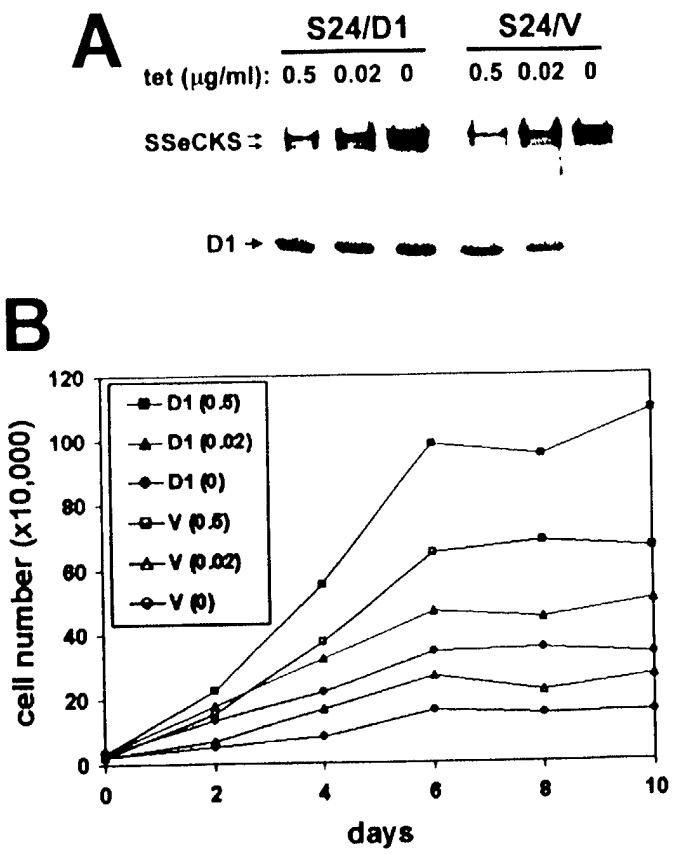

Figure 57

(87 of 90)

Figure 58

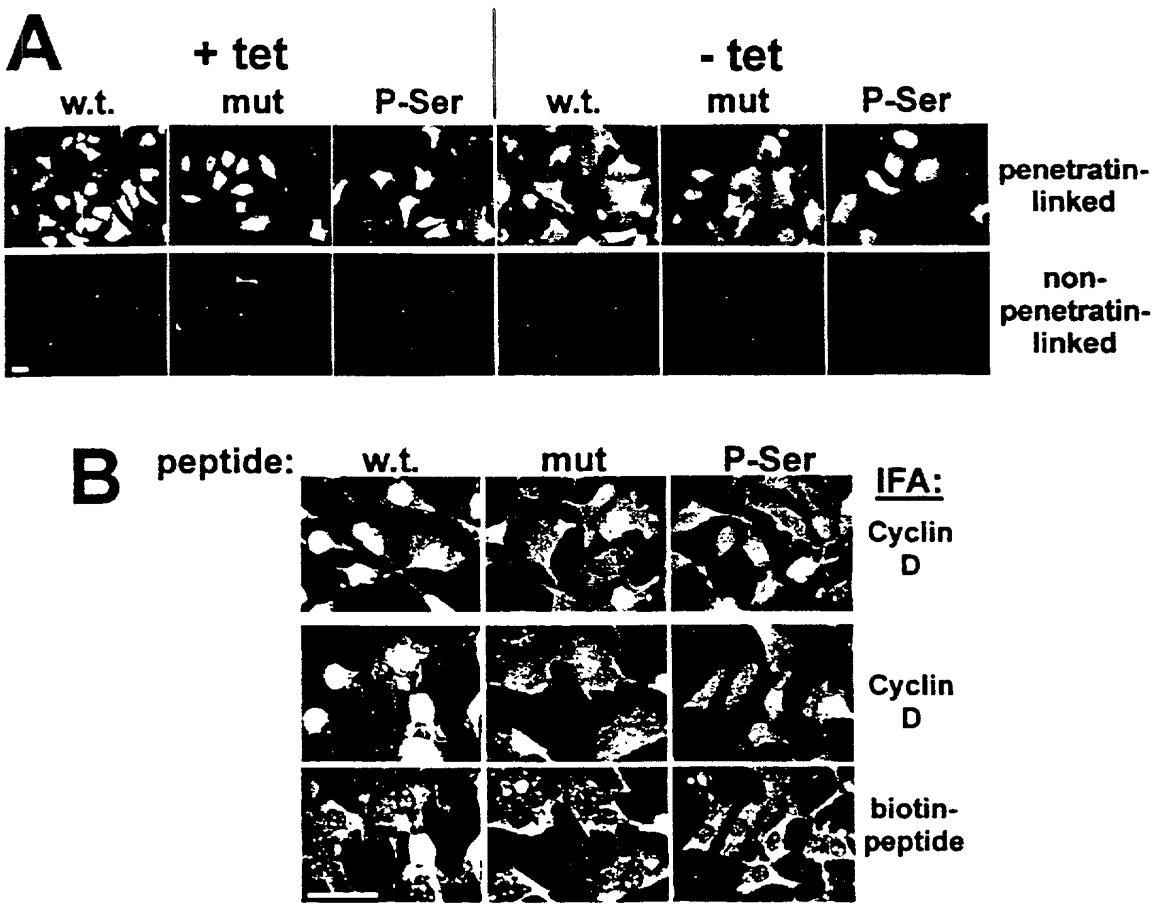
A
+ tet
- tet
w.t.
mut
P-Ser
w.t.
mut
P-Ser
penetratin-linked
non-penetratin-linked
B
peptide:
w.t.
mut
P-Ser
IFA:
Cyclin D
Cyclin D
biotin-peptide

Figure 59

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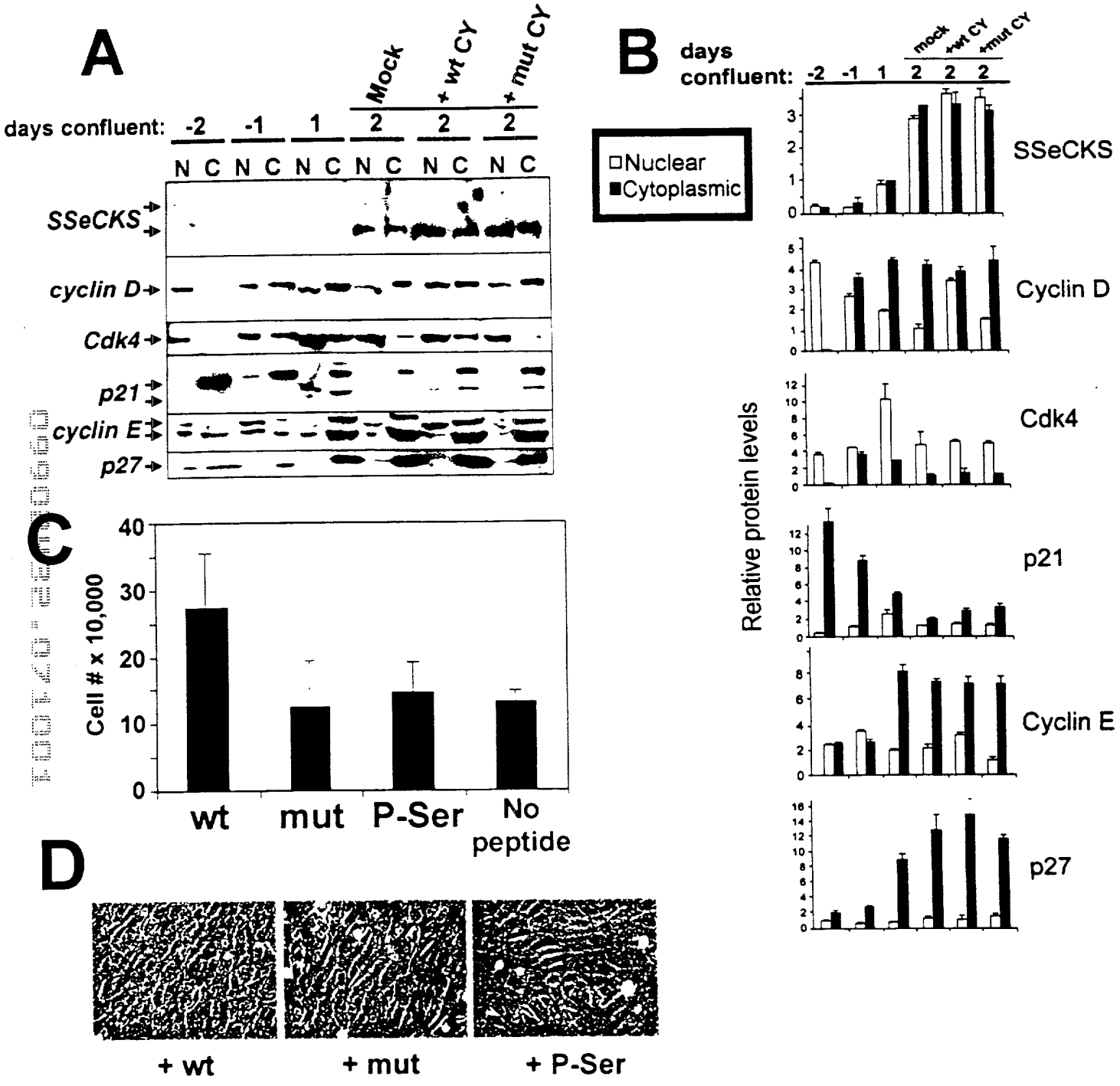

Figure 60
(90 of 90)